GenCore version 5.1.3
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Command line parameters:

-MODEL-framet_p2n.model -DEV-xlh
-MODEL-framet_p2n.model -DEV-xlh
-Q-/Ggn2_1/USPTO_Spool/US09697089/runat_29012003_092504_19158/app_query.fasta_1.1223
-DB-GenEmbl -QFMT-fastap -SUFFIX-p2n.rge -MINMATCH-0.1 -LOOPCL-0 -LOOPEXT-0.
-UNITS-blits -START-1 -END--1 -MATRIX-pam120 -TRANS-human40.cdi -LIST-45
-DOCALIGN-200 -THR_SCORE-pct -THR_MAX-100 -THR_MIN-0 -ALIGN-15 -MODE-LOCAL
-OUTFMY-pto -NORM-ext -HEAPSIZE-500 -MINLEN-0 -MAXLEN-2000000000
-USER-US09697089_6CGN_11_4449_@runat_29012003_092504_19158 -NCPU-6 -ICPU-3
-NO_XDFY -NO_MMAP -LARGEQUERY -NEG_SCORESO - WAIT -LONGLOG -DEV_TIMEOUT-120
-WARN_TIMEOUT-30 -THREADS-1 -XGAPEXT-7
-YGAPOP-4 -YGAPEXT-12 -DELOP-6 -DELEXT-7
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_mus:*
34: em_htg_mus:*
34: em_htg_pin:*
35: em_htg_pin:*
36: em_htg_pin:*
37: em_htg_vrt:*
38: em_sy:*
40: em_htg_o_hum:*
41: em_htg_o_ther:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| 37 38 39 40 41 42 42 43 | c 31 30 33 33 34 | 0 0 0 0 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 | 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | Result |
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| 5. | | л <i>.</i> | 1 00 00 00 00 00 00 00 00 00 00 00 00 00 | Query Match |
| 5366 5366 5502 5984 5984 6124 6124 | 5269 179252 165 5362 5497 196486 4013 | 578 261 107885 83866 83866 117791 41613 206808 | 3133 3360 3360 3581 3581 3356 3396 3396 3396 3396 180583 3160583 1160583 1185469 1185469 11955 1 | Length |
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| E23944 E24990 A64509 E23943 E28989 E38321 E38321 A64529 AX335820 HSU19251 | AF135495 AF135205 AF318178 AX318178 AF135491 AF007769 AC116741 AB048534 | AY027790 AX318172 AX318172 AC131423 G55568 AF24243151 AF24243351 AF24243351 | AY032589 AY035391 BC031555 AF376061 AK095467 AX318091 AY027787 CC010968 CC101793 AC101793 IF2005417 AX318174 AX318176 AX318097 AX318097 AX318097 AX318097 AX318097 AX318097 AX318097 AX318097 AX318097 AX318097 AX318097 AX318097 | ID |
| 944 Excess 990 Apoptos 509 Sequen 943 Excess 943 Excess 989 Apoptos 321 Monocl 321 Sequen 35820 Sequen 35820 Sequen | AF135492 Mus muscu AF131205 Mus muscu AF318178 Seguence AF315491 Mus muscu AF007769 Mus muscu AF0176741 Mus muscu AC116741 Mus muscu AB048534 Homo sapi | Homo Seque Seque Rattu Rattu SHGC-1 Mus Mus Rattu | AY032589 Homo sapi AY035391 Homo sapi BC031555 Homo sapi AF376061 Homo sapi AK095467 Homo sapi AX318091 Sequence AY027787 Homo sapi AC010968 Homo sapi AL121653 BAC seque AC101793 Mus muscu AL1389934 Homo sapi AX318093 Sequence AX318174 Sequence AX318174 Sequence AX318175 Sequence AX318176 Sequence AX318097 Sequence AX318097 Sequence AX0277789 Homo sapi AL121658 BAC sequence AX011232 Homo sapi AX318095 Sequence | Description |

275 80 215 60

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MKTPLFVVITCAIQMGESEFHSHTOTTLFHTBYDLLIQKMKHKHKGVAASDFIRSLDH
GGDLALEGVESHKFDEFLQDVSSVNEDVLLTTGLLCKYTAQRFKRKYKFFHKSFQEYT
AGRRLSSLLTSHEPEEVTKGNGYLQKMVSISDITSTYSSLLRYTGGSSVEATRAVMKH
LAAVYQHGCLLGLSIAKRPLMRQESLQSVKNTTEQEILKAININSFVECGIHLYQEST
SKSALSQEFEAFFQGKSLYINGSNIPDYLEDFFEHLPNCASALDFIKLDFYGGAMASW
EKAAEDTGGIHMEEAPETY1PSRAVSLFFNWKQEFTLEVTLRDFSKLNKQDITYLGK
IFSSATSLRLQIKRCAGVAGSLSLVLSTCKNIYSLMVEASPLTIEDERHITSVTNLKT
LSIHDLQNQRLPGGLTDSLGNLKNLTKLIMDNIKMNEEDAIKLAEGLKKNLKKMCLEHL
THLSDIGGMDYIVKGSLSSEPCDLEEIQLVSCCLSANAVKILAGNLKHLEEVPQLVKLGI
KNRRLTDTEIRILGAFFGKNPLKNEQQLNLAGNRVSSDGALAFMGVFENLKGLVFEDF
KNRRLTDTEIRILGAFFGKNPLKNEQQLNLAGNRVSSDGALAFMGVFENLKGLVFEDF
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2001. .3107
/note="LRR;
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/protein_id="AAK38730.1"
/protein_id="AAK38730.1"
/db_xref="07:13899173"
/translation="MNFIKDNSRALIQRMGMTVIKQITDDLFVWNVLNREEVNIICCE
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LQSPCIIEGESGKGKSTLLQRIAMLWGSGKCKALTKFKFVFFLRLSRAQGGLFETLCD
QLLDIPGTIRKQTFWAMLLKLRQRVLFLLDGYNEFKPQNCPEIEALIKENHRFKNWYI
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/note="CARD;
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/db_xref="taxon:9606"
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REFERENCE

Homo sapiens. Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 3219)

| RESULT 2 AY035391 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM | Qy 1021 Db 3096 | Qy 1001 рь 3036 | Qy 981 Db 2976 | Qy 961 Db 2916 | Qy 941 Db 2856 | Qy 921 Db 2796 | Qy 901 Db 2736 | Qy 881 Db 2676 | Qy 861 Db 2616 | Qy 841 Db 2556 | Qy 821 Db 2496 | Qy 80: Db 243 | 7 8 | Qy 76 Db 231 | Qy 74 Db 225 |
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| AY035391 N Homo sapiens ICE-protease activating factor mRNA, complete cds. AY035391 AY035391 AY035391.1 GI:14334214 Homo sapiens Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleogromi. | LeuvalThrala 1024 CTAGTAACTGCT 3107 | ArgLeuValGlyTrpGlnPheAspAspAspAspLeuSerValIleThrGlyAlaPheLys 1020 | ProAlaLeuValArgLysLeuSerGlnValLeuSerLysLeuThrPheLeuGlnGluAla 1000 | PheGluAsnLeuLysGinLeuValPhePheAspPheSerThrLysGluPheLeuProAsp 980 | GInLeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTrpLeuAlaPheMetGlyVal 960 | ASPThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPheGln 940 | LysHisLeuGluGluValProGlnLeuValLysLeuGlyLeuLysAsnTrpArgLeuThr 920 | L LeuThrAlaLeuMetLeuProTrpGlyCysAspValGlnGlySerLeuSerSerLeuLeu 900 | GluLysAspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGluGln 880 | l AlaGlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeu 860 | 1 AspLeuGluGluIleGlnLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeu 840 | 1 LeuSerAspIleGlyGluGlyMetAspTyrIleValLysSerLeuSerSerGluProCys 820 | 1 IleLysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHis 800 | 1 AsnLeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluGluAspAla 780 | 1 LeuSerIleHisAspLeuGlnAsnGlnArgLeuProGlyGlyLeuThrAspSerLeuGly 760 |

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Poyet, J.L., Srinivasula, S.M., Thani, M., Razmara, M., Fernandes-Alnemri, T. and Alnemri, E.S. Identification of Ipaf, a human caspase-1-activating related to Apaf-1 J. Biol. Chem. 276 (30), 28309-28313 (2001) 213594.54
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QLLDIFGTIRKOTFMAMILKLRORVLFILDGYNEFKPQNCPEIEALIKENHFFKNMVI
VTTTTECLRHTROFGALTAEVCDMTEDSAQALIREVLAKELARGLLLOJOKSRCLRNL
MKTPLFVVITCAIQMGESEFHSHTQTTLFHTFYDLLIGKNKHKHKGVAASDFIRSLDH
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LAAVYQHGCLLGLSIAKRPLWROESLGSVKNTTEQEILKAININISFYCEGIHLYQEST
SKSALSGEFEAFFGGKSIYINSGNIPDYLFDFFEHLPNCASALDFIKLDFYGGAMASW
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THISDIGEGMDYIVKSLSSEPCDLEEIQLVSCCLSANAVKILAQNLHNLVKLSILDLS
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                      1404
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| 20 (| euSerAspIleGlyGluGlyMetAspTyrIleValLysSerLeuSerSerGluProCys | 80 | 4 |
|--------------|--|-------------|---------|
| 800 2544 | IleLysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHis | 781 2485 | B 6 |
| 780 | ASnLeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluGluAspAla | 761 | ρ |
| 2484 | | 2425 | Q |
| 760 2424 | rlleHisAspLeuGlnAsnGlnArgLeuProGlyGlyLeuThrAspSerLeuGly | | 유 양 |
| 740 | AlaSerProLeuThrIleGluAspGluArgHisIleThrSerValThrAsnLeuLysThr | 721 | β |
| 2364 | | 2305 | δ |
| 720 | AlaGlySerLeuSerLeuValLeuSerThrCysLysAsnIleTyrSerLeuMetValGlu | 701 | B & |
| 2304 | | 2245 | |
| 700 | GlyLysIlePheSerSerAlaThrSerLeuArgLeuGlnIleLysArgCysAlaGlyVal | 681 | B 8 |
| 22 44 | | 2185 | |
| 680 | ThrLeuGluValThrLeuArgAspPheSerLysLeuAsnLysGlnAspIleThrTyrLeu | 661 | B 6 |
| 2184 | | 2125 | |
| 660 | GluThrTyrIleProSerArgAlaValSerLeuPhePheAsnTrpLysGlnGluPheArg | 641 | В |
| 212 4 | | 2065 | 8 |
| 640 | MetAlaSerTrpGluLysAlaAlaGluAspThrGlyGlyTleHiSMetGluGluAlaPro | 621 | β |
| 2064 | | 2005 | δ |
| 620 | H1sLeuProAsnCysAlaSerAlaLeuAspPheIleLysLeuAspPheTyrGlyGlyAla | 601 | д |
| 2004 | | 1945 | В |
| 600 | GlyLysSerLeuTyrIleAsnSerGlyAsnIleProAspTyrLeuPheAspPhePheGlu | 581 | D |
| 1944 | | 1885 | Qy |
| 580 | LeuTyrGlnGluSerThrSerLysSerAlaLeuSerGlnGluPheGluAlaPhePheGln | 561 | B |
| 1884 | | 1825 | 64 |
| 560 1824 | ThrGluGlnGluIleLeuLysAlaIleAsnIleAsnSerPheValGluCysGlyIleHis | 541 1765 | 유 |
| 540 | LeuSerIleAlaLysArgProLeuTrpArgGlnGluSerLeuGlnSerValLysAsnThr | 521 | 망양 |
| 1764 | | 1705 | |
| 520 1704 | AlaThrArgAlaValMetLysHisLeuAlaAlaValTyrGlnHisGlyCysLeuLeuGly | - | B 6 |
| 500 | SerAspIleThrSerThrTyrSerSerLeuLeuArgTyrThrCysGlySerSerValGlu | | g |
| 1644 | | | 9 |
| 480 1584 | SerHisGluProGluGluValThrLysGlyAsnGlyTyrLeuGlnLysMetValSerIle | 1525 | g Vo |
| 460 1524 | PhePheHisLysSerPheGlnGluTyrThrAlaGlyArgArgLeuSerSerLeuLeuThr | ь | B 6 |

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REMARK
COMMENT
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AUTHORS
TITLE
JOURNAL
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ORGANISM
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTCACCGCACTGATGCTGCCCTGGGGCTGTGACGTGCAAGGCAGCCTGAGCAGCCTGTTG
                                                                      Strausberg, R.
Strausberg, R.
Strausberg, R.
Direct Submission
Direct Submission
Submitted (06-JUN-2002) National Institutes of Health, Mammalian Submitted (06-JUN-2002) Cancer Genomics Office, National Cancer Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
NHH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (
DNA Sequencing by: Baylor College of Medicine Human
                                                                                                                                                            Eukaryota;
Mammalia; E
                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 3360)
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                                                                                                                                                                                 Homo sapiens
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Primates;
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                                                                                                                                                            Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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Pred. No.:
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Best Local Similarity:
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                                       352
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61
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LysGlySerGluSerCysAsnLeuPheLeuLysSerLeuLysGluTrpAsnTyrProLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequencing Center
Center code: BCM-HGSC
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Contact: amg@bcm.tmc.edu
Contact: amg@bcm.tmc.edu
Contact: A.M., Lu, X., Hulyl
Yoon, V.S., Kowis, C.R., Lawrence, S., Martt
Richards, S., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1011
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LQSPCIIEGESGKKSTLLQARTAMLWGSGKCRALTKKEVYFFLALSKELLQA
LQSPCIIEGESGKKSTLLQARTAMLWGSGKCRALTKKEVPFLALSKELLQOLOKSRCLRNL
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CGDLALEGVFSHKFDFELQDVSSVNEDVLLTTGLLCKYTAQRFKRYKFFHKSFQEYT
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LAAVYQHGCLLGLSIAKRPLWROESLOSVKNTTEOEILKAININSFVECGIHLYQEST
SKSALSQEFEAFFGGKSLYINSGNIFDYLFDFFFHLHNCASALDFIKLDFYGGAMASW
EKAAEDTGGIHMEEAPETYIPSRAVSLFFNWKQEFRTLEVTLRDFSKLMKQDIRYLGK
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LSIHDLQORLDGGLTDSLGNLKNLTKILIMDNIKMNEEDAIKLAGLKHLEKUCLFHL
THLSDIGEGMDYIVKSLSSEPCDLEEIQLVSCCLSANAVKILAQNLHNLVKLSILDLS
ENYLEKDGNEALHELIDRMNVLEQLTALMLPWGCDVGGSLSSLLKHLEEVPQLVKKGL
KNWRLDTDEIRTLGAFFGKNUPLKNFGLTMALMLPWGCDVGGSLSSLLKHLEEVPQLVKKGL
KNWRLDTDEIRTLGAFFGKNUPLKNFGLTMALMLPWGCDVGGSLSSLKALKKULYFEDF
STKEFLPDPALVRKLSQVLSKLITFLQEARLVGWGFDDDDLSVITGAFKLVTA"

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/clone="mgc:35330 IMAGE:5179909"
/tissue_type="Brain, Lung, Testis
/clone_lib="NHH_MGC_115"
/lab_host="DH10B"
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Gingras, M.-C., Qiu, J. and Margolin, J.F.
Differential expression of the caspase recruitment
12 (CARD12) during monocytic differentiation
Unpublished
    2 (bases 1 to 3581)
Gingras,M.-C., Qiu,J. and Margolin,J.F.
Direct Submission
Submitted (03-MAY-2001) Pediatric/Texas
Baylor College of Medicine, 6621 Fannin
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                                                                                       Homo sapiens
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Kodaira,H., Furuya,T., Takahashi,M., Kilkawa,E., Omura,Y.,
Kamihara,K., Katsuta,N., Sato,K., Tanikawa,M., Yamazaki,M.,
Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Wakamatsu,A., Ishii,S.,
Yamamoto,J., Isono,Y., Kawai-Hio,Y., Sato,K., Nishikawa,T.,
Kimura,K., Yamashita,H., Matsuo,K., Nakamura,Y., Sekine,M.,
Kikuchi,H., Murakawa,K., Kanehori,K., Takahashi-Fujii,A.,
Shima,A., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S.,
Nagahari,K., Masuho,Y., Nagai,K., and Isogai,T.
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/cell_type="CD34+ Cells"
/clone_lib="D9OST2"
/clone_ib="D9OST2"
/note="cloning vector: pME18SFL3-mRNA from CD34+ cells
after 9-days ODF induction.-primary culture, CD34+ Cells"
a 726 c 774 g 869 t
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| Db Qy | 982 261 | AGAGGGTTCTTTTCCTTCTTGATGGCTACAATGAATTCAAGCCCCAGAACTGCCCAG leGluAlaLeuIleLysGluAsnHisArqPheLysAsnMetValIleValThrThrT | 1041 |
|----------|------------|--|------|
| ДЪ | 1042 | AAGCCCTGATAAAGGAAAACCACCGCTTCAAGAACATGGTCATCGTCACCACTAC | 1101 |
| Qy | 281 | hrGluCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAsph | 300 |
| рь | 1102 | AGTGCCTGAGGCACATACGGCAGTTTGGTGCCCTGACTGCTGAGGTGGGGGATAT | 1161 |
| Qy | 301 | hrGluAspSerAlaGlnAlaLeuIleArgGluValLeuIleLysGluLeuAlaGluG | 320 |
| Db | 1162 | ACAGAAGACAGCGCCCAGGCTCTCATCCGAGAAGTGCTGATCAAGGAGCTTGCTGAAGGC | 1221 |
| Qy | 321 | euLeuLeuGlnIleGlnLysSerArgCysLeuArgAsnLeuMetLysThrProLeuF | 340 |
| DЬ | 1222 | TTGCTCCAAATTCAGAAATCCAGGTGCTTGAGGAATCTCATGAAGACCCCTCTCTT | 1281 |
| Qy | 341 | rCysAlaIleGlnMetGlyGluSerGluPheHisSerHisThrGlnT | 360 |
| Db | 1282 | TGGTCATCACTTGTGCAATCCAGATGGGTGAAAGTGAGTTCCACTCTCACACACA | 1341 |
| Qy | 361 | LeuPheHisThrPheTyrAspLeuLeuIleGlnLysAsnLysHisLysHisLysGl | 380 |
| Дb | 1342 | GCTGTTCCATACCTTCTATGATCTGTTGATACAGAAAAACAAAC | 1401 |
| Qγ | 381 | alAlaAlaSerAspPheIleArgSerLeuAspHisCysGlyAspLeuAlaLeuGluGl | 400 |
| DЬ | 1402 | GTGGCTGCAAGTGACTTCATTCGGAGCCTGGACCACTGTGGAGACCTAGCTCTGGAGGGT | 1461 |
| Qy | 401 | alPheSerHisLysPheAspPheGluLeuGlnAspValSerSerValAsnGluAspVal | 420 |
| Db | 1462 | FTCTCCCACAAGTTTGATTTCGAACTGCAGGATGTGTCCAGCGTGAATGAGGATGT | 1521 |
| Qy | 421 | LeuLeuThrThrGlyLeuLeuCysLysTyrThrAlaGlnArgPheLysProLysTyrLys | 440 |
| Db | 1522 | TGCTGACAACTGGGCTCCTCTGTAAATATACAGCTCAAAGGTTCAAGCCAAAGTATAAA | 1581 |
| Оу | 441 | PheHisLysSerPheGlnGluTyrThrAlaGlyArgArgLeuSerSerLeuLeuThr | 460 |
| Дb | 1582 | TCTTTCACAAGTCATTCCAGGAGTACACAGCAGGACGAAGACTCAGCAGTTTATTGA | 1641 |
| Qy | 461 | rLeuGlnLysMetValSerIle | 480 |
| Db | 1642 | CTCATGAGCCAGAGGAGGTGACCAAGGGGAATGGTTACTTGCAGAAAATGGTTTCCATT | 1701 |
| Qy | 481 | TyrSerSerLeuLeuArgTyrThrCysGlySerSerValGlu | 500 |
| Db | 1702 | CGGACATTACATCCACTTATAGCAGCCTGCTCCGGTACACCTGTGGGTCATCTGTGGAA | 1761 |
| Qy | 501 | ThrArgAlaValMetLysHisLeuAlaAlaValTyrGlnHisGlyCysLeuLeuGly | 520 |
| Дb | 1762 | CCACCAGGGCTGTTATGAAGCACCTCGCAGCAGTGTATCAACACGGCTGCCTTCTCGG | 821 |
| Qy | 521 | oLeuTrpArgGlnGluSerLeuGlnSerValLysAsnThr | 540 |
| Db | 1822 | TTTCCATCGCCAAGAGGCCTCTCTGGAGACAGGAATCTTTGCAAAGTGTGAAAAAAAA | 1881 |
| Qy | 541 | ThrGluGlnGluIleLeuLysAlaIleAsnIleAsnSerPheValGluCysGlyIleHis | 560 |
| Db | 1882 | CTGAGCAAGAATTCTGAAAGCCATAAACATCAATTCCTTTGTAGAGTGTGGCATCCAT | 1941 |
| Qy | 561 | SerLysSerAlaLeuSerGlnGluPheGluAlaPhePheGln | 580 |
| Дb | 1942 | TATATCAAGAGAGTACATCCAAATCAGCCCTGAGCCAAGAATTTGAAGCTTTCTTT | 2001 |
| Qy | 581 | GlyLysSerLeuTyrIleAsnSerGlyAsnIleProAspTyrLeuPheAspPhePheGlu | 600 |
| Db | 2002 | GTAAAAGCTTATATATCAACTCAGGGAACATCCCCGATTACTTATTTGACTTCTTTGAA | 2061 |
| Qy | 0 | HisLeuProAsnCysAlaSerAlaLeuAspPheIleLysLeuAspPheTyrGlyGlyAla | 620 |
| Db | 2062 | ATTTGCCCAATTGTGCAAGTGCCCTGGACTTCATTAAACTGGACTTTTATGGGGGAGCT | 2121 |

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                                     GlnLeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTrpLeuAlaPheMetGlyVal 960
                                                                  AspThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPheGln
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GATACAGAGATTAGAATTTTAGGTGCATTTTTTGGAAAGAACCCTCTGAAAAACTTCCAG
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TTTGAGAATCTTAAGCAATTAGTGTTTTTTGACTTTAGTACTAAAGAATTTCTACCTGAT
                             GACCTTGAAGAAATTCAATTAGTCTCCTGCTGCTTGTCTGCAAATGCAGTGAAAATCCTA
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Patent: WO 0190156-A 96 29-NOV-2001;
The Burnham Institute (US)
Location/Qualifiers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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| 380 1416 | i ThrLeuPheHisThrPheTyrAspLeuLeuIleGlnLysAsnLysHisLysHisLysGly | 36 135 | Qу рь |
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| 360 1356 | ValValIleThrCysAlaIleGlnMetGlyGluSerGluPheHisSerHisThrGlnThr | 34 129 | Фр |
| 340 1296 | <pre>21 LeuLeuLeuGlnIleGlnLysSerArgCysLeuArgAsnLeuMetLysThrProLeuPhe </pre> | 32 123 | Db Qy |
| 320 1236 |)1 ThrGluAspSerAlaGlnAlaLeuIleArgGluValLeuIleLysGluLeuAlaGluGly | 30 117 | Дy |
| 300 1176 | 31 ThrGluCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMet | 28 111 | Db Oy |
| 280 1116 | 51 IleGluAlaLeuIleLysGluAsnHisArgPheLysAsnMetValIleValThrThrThr | 26 105 | B 64 |
| 260 1056 | 1 GlnArgValLeuPheLeuLeuAspGlyTyrAsnGluPheLysProGlu | 24 99 | DP OA |
| 240 996 | 1 LeuAspIleProGlyThrIleArgLysGlnThrPheN | 93 93 | 94 VQ |
| 220 936 |)1 PhePheLeuArgLeuSerArgAlaGlnGlyGlyLeuPheGluThrLeuCysAspGlnLeu | 20 87 | Оу |
| 200 876 | 1 ArgIleAlaMetLeuTrpGlySerGlyLysCysLysAlaLeuThrLysPheLysPheVal | 18 81 | Db Qy |
| 180 816 | 11 LeuGlnSerProCysIleIleGluGlyGluSerGlyLysGlyLysSerThrLeuLeuGln | 16 75 | gb Qy |
| 160 756 | 11 ArgLysAspGlnHisHisHisArgValGluGlnLeuThrLeuAsnGlyLeuLeuGlnAla | 14 69 | Дb |
| 140 696 | 1 GlyGluAspIleAspIleIlePheAsnLeuLysSerThrPheThrGluProValLeu | 12 63 | Qy db |
| 120 636 |)1 LeuAlaGlnAspLeuLysAspLeuTyrHisThrProSerPheLeuAsnPheTyrProLeu | 10 57 | Qу |
| 100 576 | 31 PheGlnAspLeuAsnGlyGlnSerLeuPheHisGlnThrSerGluGlyAspLeuAspAsp | 51 | Дb |
| 80 516 | 11 LysGlySerGluSerCysAsnLeuPheLeuLysSerLeuLysGluTrpAsnTyrProLeu | 4 6 | Оy |
| 60 456 | il IleCysCysGluLysValGluGlnAspAlaAlaArgGlyTleIleHisMetTleLeuLys | 39 | Ф |
| 40 396 | 1 LysGlnIleThrAspAspLeuPheValTrpAsnValLeuAsnArgGluGluValAsnIle | 3 3 2 | Qy Db |

| 10111111111111111111111111111111111111 | | euSerIleHisAspLeuGlnAsnGlnArgLeuProGlyGlyLeuThrAsp | 7 | Ωу |
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| 401 valpheSerHistyspheAsppheGlutendining | 740 | GluargHisIleThrSerValThrAsnLeuLysTh | ü N | Оу |
| | 720 | laGlySerLeuSerLeuValLeuSerThrCysLysAsnIleTyrSerLeuMetValGl | 70 37 | ФФ |
| 1417 GTGGCTGCAAGTGCTTCATTCGGACCCTGGACACCACGTGGAGACCACGTCGAGGGGGT 147 401 ValpheSerHistysPheAsppheGluLeuGlnAspValSerSerValAsnGluAspVal 420 1477 GTGTTCTCCCCACAGTTTCATTCGGACCTGGGAGACCACGTGGAGACCTAGGCTTGATGGGGGT 147 421 LeuLeuThrThrGlyLeuleuGysLysTyrThrAlaGlnArgpheLysProLysTyrLys 40 147 PhePheHistySSerPheGlnGluTyrThrAlaGlnArgpheLysProLysTyrLys 40 1537 CTGCTGACAACTGGGCTCCTCTGTAAATATACAGCTCAAAGTTCAACCTACACAACTGACAACTGGACTTCAACGTTCAAAGTTCAACTGACCAACTGACACTACAACTGCAACTACACTCAAGTTCAAACTGCAAGTACAACTGCAACTACACCAACTACACCAACTACACCAACTACACCAACTACACCAACTACACCAACTACACCAACTACACCAACTACACCAACTACACCAACTACACCAC | 700 | lyLysIlePheSerSerAlaThrSerLeuArgLeuGlnIleLysArgCysAlaGlyVa | 31 | Qу |
| 1417 GTGGCTGCAAGTGGCTTCATTGGGGCCTGGAACCACGTGGGGACCCTGGGGGACCACGTCTGGAGGGCTCTGAAGGCTTGAAGGCTTGAAGGCTTGAAGGCTTGAAGGCTTGAAGGCTTGAAGGCTTGAAGGCTTGAAGGCTTGAAGGCTTGAAGGCTTGAAGGCTTGAAGGCTTGAAGGCTTGAAGGCTTGAAGGCTTGAAGGTTCAAGGCTTGAAGGTTCAAAGTATAAATATAAAGCAAGAAGGAGAGAGA | 680 231 | rLeuGluValThrLeuArgAspPheSerLysLeuAsnLysGlnAspIleThrTyrLe | 25 | Qy Db |
| 1417 GTGGCTGCAAGTGACTTCATTTGGAGCCTGGACCACGTTGGAAGACTAGCCTTGAAGGGT 147 1417 GTGGCTGCAAGTGACTTCATTTGGAGCCTGGACCACGTTGGAAGACTAGCCTTGAAGGGT 147 141 ValpheserHisLyspheAsppheGluLeuGlnAspValSerSerValAsnGlnAspVal 142 LeuLeuThrThrGlyLeuLeuCysLysTyrThrAlaGlnArgPheLysProLysTyrLys 143 CTGCTGCACAAGTTTGATTTCGAACTGCAGGATTGTCAAGCTTCAAGCTTCAAGCTTAAGCTTAAGCTTCAAGCTTAAGCTTAAGCTAAGCTTAAGCTAAGCTAAGCTTAAGCAAGTTTTGATTTCAAGCTGCAAGGATTCAAGCTTAAGCAAGTTTAAGCAGATTTTGATTTCAAGCTAAGCTAAAGCTAAAGCTCAAGCAAG | 225 | luThrTyrIleProSerArgAlaValSerLeuPhePheAsnTrpLysGlnGluPheAr | 64 19 | Qy Db |
| | 640 | AlaSerTrpGluLysAlaAlaGluAspThrGlyGlyIleHisMetGluGluAlaPr | 62 | Db Qy |
| 1417 GYGGCTGCAAGTGACTTCATTGGAGCCTGGAGCCCCGTGGAGACCTAGCTCTGGAGGGT 147 1417 GYGGCTGCAAGTGACTTCATTGGAGCCTGGAGCCACCGTGGAGACCTAGCTCTGGAGGGT 147 1411 GYGGCTGCAAGTTATTTGGATTTGGAACTGCAGGATGTGTGTCCAGGATGTCTTGGAGGATGTCAACTCTGGAGGGT 147 1411 HILLIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHI | 213 | isLeuProAsnCysAlaSerAlaLeuAspPheIleLysLeuAspPheTyrGlyGlyAl | 60 07 | ДУ |
| 1417 GTGGCTGCAAGTGCATTCGGAGCCTGGACCACGTGGAGACCTAGCTTGGAGGTT 147 401 ValpheSerHisLysPheAspPheGluLeuGlnAspValSerSerValAsnGluAspVal 420 401 ValpheSerHisLysPheAspPheGluLeuGlnAspValSerSerValAsnGluAspVal 420 411 LeuLeuThrThrGlyLeuLeuCysLysTyrThrAlaGlnArgPheLysProLysTyrLys 440 421 LeuLeuThrThrGlyLeuLeuCysLysTyrThrAlaGlnArgPheLysProLysTyrLys 440 421 LeuLeuThrThrGlyLeuLeuCysLysTyrThrAlaGlnArgPheLysProLysTyrLys 440 421 LeuLeuThrThrGlyLeuLeuCysLysTyrThrAlaGlnArgPheLysProLysTyrLys 440 422 LeuLeuThrThrGlyLeuLeuCysLysTyrThrAlaGlnArgPheLysProLysTyrLys 440 433 CTGCTGACAACTGGGCTCCTCTGTAAATATACAGCTCAAAGGTTCAAGCCAAAGTATAAA 159 441 PhePheHisLysSerPheGlnGluTyrThrAlaGlnArgArgLeuSerSerLeuLeuThr 460 441 PhePheHisLysSerPheGlnGluTyrThrAlaGlnArgArgLeuSerSerLeuLeuThr 460 441 PhePheHisLysSerPheGlnGluTyrThrAlaGlnArgArgCaAGCCAAAGTTTATTGACG 451 SerHisGluProGluGluValThrLysGlySanGlyTyrLeuGlnLysMetValSerIle 460 461 SerHisGluProGluGluValThrLysGlyAsnGlyTyrLeuGlnLysMetValSerIle 460 462 SerHisGluProGluGluValThrLysGlyAsnGlyTyrLeuGlnLysMetValSerIle 460 463 SerHisGluProGluGluValThrLysGlyTyrLeuGlnLysMetValSerIle 460 464 SerHisGluProGluGluValThrLysGlyTyrLeuGlnLysMetValSerIle 460 465 TCTCATGAGCCAGAGGGTGACCAAGGGGGGAATGTTTGTGAAAATGGTTTCCATT 177 481 SerAspIleThrSerThrTyrSerSerLeuLeuArgTyrThrCysGlySerSerValGlu 500 481 SerAspIleThrSerThrTyrSerSerLeuLeuArgTyrThrCysGlySerSerValGlu 500 481 SerAspIleThrArgAlaYalmetLysHisLeuAlaAlaValTyrGlnHisGlyCysLeuLeuGly 520 481 SerAspIleThrArgAlaYalmetLysHisLeuArgCargCargCargCargCargCargCargCargCargCa | 600 207 | lyLysSerLeuTyrIleAsnSerGlyAsnIleProAspTyrLeuPheAspPhePheO | 58 | Qy Qy |
| 11111111111111111111111111111111111111 | 580 | euTyrGlnGluSerThrSerLysSerAlaLeuSerGlnGluPheGluAlaPhePheGl | G O | Дy |
| 11111111111111111111111111111111111111 | 560 195 | hrGluGlnGluIleLeuLysAlaIleAsnIleAsnSerPheValGluCysGlyIleHi | 4 9 | Дy |
| 11111111111111111111111111111111111111 | 189 | euSerIleAlaLysArgProLeuTrpArgGlnGluSerLeuGlnSerValLysAsnTh | 83 | Дy |
| 11111111111111111111111111111111111111 | 520 183 | .laThrArgAlaValMetLySHi\$LeuAlaAlaValTyrGlnHi\$GlyCysLeuLeuGl | 50 77 | Фф |
| 1417 GTGGCTGCAAGTGACTTCATTCGGAGCCTGGACCACCGTGGAGCCTAGCTCTGGAGGGT 147 401 valpheSerHisLysPheAspPheGluLeuGlnAspValSerSerValAsnGluAspVal 1477 GTGTCTCCCACAAGTTTGATTCGAAGTGCAGGAGCTGGAGGGTCTGGAGGGT 147 421 LeuLeuThrThrGlyLeuLeuCysLysTyrThrAlaGlnArgPheLysProLysTyrLys 421 LeuLeuThrThrGlyLeuLeuCysLysTyrThrAlaGlnArgPheLysProLysTyrLys 421 LeuLeuThrThrGlyLeuLeuCysLysTyrThrAlaGlnArgPheLysProLysTyrLys 421 CTGCTGACAAGTTGGAGCTCCTCTGTAAATATACAGCTCAAAGGTTCAAGCCAAAGTATAAA 1537 CTGCTGACAACTGGGCCTCCTGTAAATATACAGCTCAAAGGTTCAAGCCAAAGTATAAA 1597 TTCTTTCACAAGTCATTCCAGGAGTACACAGCAGGAAGACTCAGCAAGTTAATTGACG 1611111111111111111111111111111111111 | 500 177 | erAspIleThrSerThrTyrSerSerLeuLeuArgTyrThrCysGlySerSerValG | 48 | Db Qy |
| 1417 GTGGCTGCAAGTGACTTCCAGGAGTTCATTCCAGGAGTAGACCAAGGACCTCAGCAGTTTATTGACG 165 401 ValpheSerHisLyspheAsppheGluLeuGlnAspValSerSerValAsnGluAspVal 420 401 ValpheSerHisLyspheAsppheGluLeuGlnAspValSerSerValAsnGluAspVal 420 1477 GTGTTCTCCACAAGTTTGATTTCGAACTGCAGGATGTGTCCAGCGTGAATGAGGATGTC 153 421 LeuLeuThrThrGlyLeuLeuCysLysTyrThrAlaGlnArgPheLysProLysTyrLys 440 1111111111111111111111111111111111 | 480 171 | erHisGluProGluGluValThrLySGlyAsnGlyTyrLeuGlnLysMetValSerI1 | 65 | Db Qy |
| 1417 GTGGCTGCAAGTGACTTCGTTAAATATATACAGCTCAAAGGTTCAAGCCCAAAGTATAAA 159 | 460 165 | hePheHisLysSerPheGlnGluTyrThrAlaGlyArgArgLeuSerSerLeuLeuTh | .59 | Db Qy |
| 1417 GTGTTCTCCCACAAGTTTGATTTCGAACTGCAGGATGTCCCAGCGTGAAGGGTGTC 153 1477 GTGTTCTCCCACAAGTTTGATTTCGAACTGCAGGATGTCTCAAGGAGGGTGTCAAGGAGGGTGTCAGGAGGGTGTGTGGAGGGTTAGATTTCGAACTGCAGGATGTGTCCAGGGGTGAACTGAGGATGTCCCAGCGTGAATGAGGATGTC 153 | 159 | uLeuThrThrGlyLeuLeuCysLysTyrThrAlaGlnArgPheLysProLysTyrLy | 53 | Db |
| 1417 GTGGCTGCAAGTGACTTCATTCGGAGCCTGGACCACCGTGGAGACCTAGCTCTGGAGGGT 147 | 153 | alPheSerHisLysPheAspPheGluLeuGlnAspValSerSerValAsnGluAspVa | 40 | Qу |
| Valalaserasorbe learnserienden vs. Valabalaserien vas la | 147 | AsphnelleargSerLeuAsphiscysGlyAspLeuAlaLeuGlugt | .41 | Db Qy |

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                                                                                                                                                                                                                                                                                                                   AspThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPheGln
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 3396)
Damiano,J.S., Stehlik,C., Pio,F., Godzik,A. and Reed Clan, a novel human ced-4-like gene
                                                                             AY027787 3396 bp
Homo sapiens CLANA (CLAN1) mRNA,
AY027787
                                             Homo
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                                            sapiens.
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                                                         IleCysCysGluLysValGluGlnAspAlaAlaArgGlyIleIleHisMetIleLeuLys
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Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 (bases 1 to 3396)
Stehlik, C., Damiano, J.S.,
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                                                   LQSPCIIEGESGKGKSTLLQRIAMLWGSGKCKALTKFKFVFFLRLSRAQGGLFETLCD
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| 460 | 441 PhePheHisLysSerPheGlnGluTyrThrAlaGlyArgArgLeuSerSerLeuLeuThr | Qy |
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| 440 1596 | 421 LeuLeuThrThrGlyLeuLeuCysLysTyrThrAlaGlnArgPheLysProLysTyrLys | Ωy |
| 420 1536 | 401 ValPheSerHisLysPheAspPheGluLeuGlnAspValSerSerValAsnGluAspVal | Дy |
| 400 1476 | 381 ValalaalaSerAspPheIleArgSerLeuAspHisCysGlyAspLeuAlaLeuGluGly | Db |
| 380 1416 | 361 ThrLeuPheHisThrPheTyrAspLeuLeuIleGlnLysAsnLysHisLysHisLysGly | Оу |
| 360 1356 | 341 ValValIleThrCysAlaIleGlnMetGlyGluSerGluPheHisSerHisThrGlnThr | Дy |
| 340 1296 | 321 LeuLeuLeuGlnIleGlnLysSerArgCysLeuArgAsnLeuMetLysThrProLeuPhe | Db 04 |
| 320 1236 | 301 ThrGluAspSerAlaGlnAlaLeuIleArgGluValLeuIleLysGluLeuAlaGluGly | ρ δ |
| 300 1176 | 281 ThrGluCysLeuArgH1sIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMet | D Qy |
| 280 1116 | 261 IleGluAlaLeuIleLysGluAsnHisArgPheLysAsnMetValIleValThrThrThr | Оy |
| 260 1056 | 241 GlnärgVälLeuPheLeuLeuAspGlyTyrasnGluPheLysProGlnäsnCysProGlu | Db 04 |
| 240 996 | 221 LeuAspIleProGlyThrIleArgLySGlnThrPheMetAlaMetLeuLeuLySLeuArg | D Qy |
| 220 936 | 201 PhePheLeuArgLeuSerArgAlaGlnGlyGlyLeuPheGluThrLeuCysAspGlnLeu | р Q |
| 200 876 | 181 ArgIleAlaMetLeuTrpGlySerGlyLysCysLysAlaLeuThrLysPheLysPheVal | рь |
| 180 816 | 161 LeuGlnSerProCysIleIleGluGlyGluSerGlyLysGlyLysSerThrLeuLeuGln | Qy Db |
| 160 756 | 141 ArgLysaspGlnHisHisHisArgValGluGlnLeuThrLeuAsnGlyLeuLeuGlnAla | Оy |
| 140 696 | 121 GlyGluAspIleAspIleIlePheAsnLeuLysSerThrPheThrGluProValLeuTrp | Qу |
| 120 636 | 101 LeuAlaGlnAspLeuLysAspLeuTyrHisThrProSerPheLeuAsnPheTyrProLeu | рь 29 |
| 576 | | Ф |

| AlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuTh: | IleLysLeu ATAAAACTAC ATACTAC LeuSerAsp TTGTCTGACJ | 781 2617 801 2677 | Оу ДЬ Оу ДЬ |
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| | Alaser GCCAGT | 72 | Qу |
| SerLeuSerLeuValLeuSerThrCysLysAsnIleTyrSerLeuMetVa | AlaGly GCTGGA | 701 2377 | Qу |
| SerSerAlaThrSerLeuArgLeuGlnIleLysArgCysAlaGlyVa | 1 GlyLysIlePhes 7 GGGAAAATATTC! | 681 2317 | Qy |
| ThrLeuargAspPheSerLysLeuAsnLysGlnAspIleThrTyrLo | 1 ThrLeuGluValThrLeuAr | 661 2257 | Qy db |
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| LysSerLeuTyrIleAsnSerGlyAsnIleProAspTyrLeuPheAspPhePheGlu | GLY | 581 2017 | Оу |
| JSerThrSerLysSerAlaLeuSerGlnGluPheGluAlaPhePhe | LeuTyrGlnGlu: | 561 1957 | Оу |
| | 1 ThrGluGlnGluI | 541 1897 | Qy Db |
| eAlaLysArgProLeuTrpArgGlnGluSerLeuGlnSerValLysAs | LeuSerIleAl | 521 1837 | Оy |
| ValMetLysHisLeuAlaAlaValTyrGlnHisGlyCysLeuLe | l AlaThrArgAla GCCACCAGGGCT | 501 1777 | Qу Db |
| SplleThrSerThrTyrSerSerLeuLeuArgTyrThrCysGlySerSer | SerA TCGG | 481 1717 | Оу |
| GluGluValThrLysGlyAsnGlyTyrLeuGlnLysMetVal: | SerHisGluProG | 461 1657 | Qy Db |
| TCATTCCAGGAGTACACAGCAGGACGAAGACTCAGCAGTTTATTG | 7 TTCTTTCACAAG | 1597 | Db |

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Center: Washington University Genome Sequencing Center code: WUGSC
Web site:http://genome.wustl.edu/gsc/index.shtml
                                                                          University School of Medicine, MO 63108, USA
On Aug 18, 2000 this sequence
                                                                                             Direct Submission
Submitted (28-SEP-1999) Genome Sequencing Center, Washington
Submitted (28-SEP-1999) Genome Sequencing Center, Washington
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Waterston, R.H.
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Sequencing vector: plasmid; 41%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOTE: This is a 'working draft' sequence. It currently consists of 1 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as
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179 27158: contig of 9980 bp in len
159 27258: gap of unknown length
159 45137: contig of 17879 bp in le
138 45237: gap of unknown length
138 65522: contig of 20285 bp in le
138 65522: contig of 20285 bp in le
139 65622: gap of unknown length
139 1498: contig of 25876 bp in le
139 91598: gap of unknown length
1499 116835: contig of 25237 bp in le
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                                                                                       AsnHisArgPheLysAsnMetVallleValThrThrThrThrThrGluCysLeuArgHisIle 287
                                                                                                                                                 AlaGlnGlyGlyLeuPheGluThrLeuCysAspGlnLeuLeuAspIleProGlyThrlle
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| 747 | AspGluArgHisIleThrSerValThrAsnLeuLysThrLeuSerIleHisAspLeuGln 7 | 728 | Qy |
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| 387 | AspLeuLeuIleGlnLysAsnLysHisLysHisLysGlyValAlaAlaSerAspPheIle 3 | 368 50027 | Оу |

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                                                                                    GluGlyGluSerGlyLysGlyLysSerThrLeuLeuGlnArgIleAlaMetLeuTrpGly
                                                  ArgValGluGlnLeuThrLeuAsnGlyLeuLeuGlnAlaLeuGlnSerProCysIleIle 167
                                                                                                                                                   LeuTyrHisThrProSerPheLeuAsnPheTyrProLeuGlyGluAspIleAspIleIle
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                                     CGCGTGGAGCAGCTGAACCCTGAATGGCCTCCTGCAGGCTCTTCAGAGCCCCCTGCATCATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (18-APR-2002) Genoscope - Centre National de Seque
BP 191 1006 EVKY EFRANCE (E-mail : seqref@genoscope
- Web : WWW.genoscope.cns.fr)
On Mar 6, 2000 this sequence version replaced gi:6002386.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Spastin, a novel AAA protein, is altered of autosomal dominant spastic paraplegia Nat. Genet. (1999) In press
2 (bases 1 to 138909)
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Mammalia; Eutheria; Pr
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/db_xref="taxon:9606"
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LeuTrpArgGlnGluSerLeuGlnSerValLysAsnThrThrGluGlnGluIleLeuLys
                                              GluTyrThrAlaGlyArgArgLeuSerSerLeuLeuThrSerHisGluProGluGluVal
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                                                                                                                                                                                                                                                   TGTAAATATACAGCTCAAAGGTTCAAGCCAAAGTATAAATTCTTTCACAAGTCATTCCAG
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                                                                                                                                                                                                                                                                                                                                                     CGGAGCCTGGACCACTGTGGAGACCTAGCTCTGGAGGGTGTTCTCCCCACAAGTTTGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SerGlyLysCysLysAlaLeuThrLysPheLysPheValPhePheLeuArgLeuSerArg
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Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastlen,V., Boguslavkiy,L., Boukhqalter,B., Chapman,C., Camarata,J., Campopiano,A., Chang,J., Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S., Ferreirar,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N., Hagos,B., Heaford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A., Karatas,A., Keyls,C., LaRocque,K., Liu,G., Lawazares,R., Landers,T., Lehozky,J., Levine,R., Liu,G., MacLean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C.,
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1 (bases 1 to 185469)
Birren,B., Nusbaum,C.
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
                                                                                                                                                                                                                                                                                                                                                                                house mouse.
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                                                                                                                                                                                                                                                                                                                     Sciurognathi; Muridae;
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CE, 43 unordered
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Gardyna,S., Gord,S., Graham,L., Grand-Pierre,N., Hagos,B.,
Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A.,
Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K.,
Liu,G., MacLean,C., Macdonald,P., Major,J., Matthews,C.,
McCarthy,M., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V.,
McCarthy,M., Meldrim,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H.,
O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K.,
Phunkhang,P., Pierre,N., Raymond,C., Retta,R., Rise,C., Rogov,P.,
Roman,J., Roy,A., Schauer,S., Schupback,R., Seaman,S., Severy,P.,
Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Talamas,J.,
Tesfaye,S., Theodore,J., Topham,K., Travers,M., Vassillev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J.,
Zembek,L., Zimmer,A. and Zody,M.
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Submitted (23-NOV-2001) Whitehead Institute/MIT Center for Genome Submitted (23-NOV-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA (bases 1 to 185469)
3 (bases 1 to 185469)
Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barran,N., Bastien,V., Bloom,T., Boguslavkiy,L., Boukhgalter,B., Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A., Cook, P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Cook, A., Cooke, P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (21-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Aug 21, 2002 this sequence version replaced gi:17060568. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                      Sequencing vector: Plasmid; n/a; 100% of reads Sequencing vector: Plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 17392 bases at least Q40 Consensus quality: 17994 bases at least Q30 Consensus quality: 180012 bases at least Q20 Insert size: 168000; agarose-fp Insert size: 181269; sum-of-contigs Quality coverage: 7.1 in Q20 bases; agarose-fp Quality coverage: 6.6 in Q20 bases; sum-of-contig
                                                                                              is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                          NOTE: This is a 'working draft' sequence. It current consists of 43 contigs. The true order of the pieces
as soon as it is available and the be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center code: WIBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center: Whitehead Institute/ MIT Center for Genome Research
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61 160: gap of 100 bp 161 824: contig of 664 bp in length 825 924: gap of 100 bp 925 1843: contig of 919 bp in length

contig of 919

60:

contig of 60 bp

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14296: contig of 891 bp in 16
14297 14396: gap of 100 bp
14397 15353: contig of 957 bp in 1e
15354 15453: gap of 100 bp
15454 16520: contig of 1067 bp in 1e
16521 16620: gap of 100 bp
16621 1620: gap of 107 bp in 1e
16621 18291: contig of 1671 bp in 1en
18292 18391: gap of 100 bp
18392 19794.
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142 9041; gap of 100 bp
42 9922; contig of 881 bp
23 1022; gap of
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11459: contig of 1437 bp

23 11559: gap of 100 bp

60 12040: contig of 481 bp

41 12140: gap of 100 bp

41 13305: contig of 1165 bp
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112959: gap
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19794: contig of 1403 bp in
19794: gap of 100 bp
21659: contig of 1765 bp in
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                                                                                                                                                            http://www.iro.es e-mail enquiries: lsumoy@iro.es EURO--MAGE Consortium Contact: Auffray C CNRS UPR 420 - Genetique Moleculaire et Biologie (IFR 1221 - Rue Guy Moquet 19, Batiment G - BP 8 94801 Villejuif Cedex, FRANCE Tel: ++33-1-49 58 34 98 Fax: ++33-1-49 58 35 09
                                                                                                                                                                                                                                                                                        Recerca Oncologica (IRO), Hospital Duran i Reynals, Av. Gran Via s/n Km 2,7 L'Hospitalet de Llobregat, 08907 Barcelona, Catalunya. SPAIN Tel: ++34-93-260-7775 Fax: ++34-93-260-7776 WWW site:
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Pluvinet,R., Estivill,X.,
Direct Submission
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Unpublished
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Lehrach, H., Poustka, A. and Lundeberg, J.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                       cDNA clone.
                                                                                        IMPORTANT: This sequence represents the full insert of this IMAGE
                                                                                                         Distributors.
                                                                                                                        This clone is available
                                                                                                                                           e-mail: auffray@infobiogen.fr
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LSRAQGGLFETLCDQLLDIPGTIRKQTFMAMLLKLRQRVLFLLDGYNEFKPQNCPEIE ALIKENHRFKNMVIVTTTTECLRHIRQFGALTAEVGDMTEDSAQALIREVLIKELAEG LLLQIQKSRCLRNLMKTPLFVVITCAIQMGESEFHSHTQTTLFHTFYDLLIQKNKHKH

| 440 840 | 21 LeuLeuThrThrGlyLeuLeuCysLysTyrThrAlaGlnArgPheLysProLysTyrLys | Qy 42 Db 78 |
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| 380 | 61 ThrLeuPheHisThrPheTyrAspLeuLeuIleGlnLysAsnLysHisLysHisLysGly | Oy 36 |
| 360 | 41 ValValIleThrCysAlaIleGlnMetGlyGluSerGluPheHisSerHisThrGlnThr | Qy 34 Db 54 |
| 340 540 | 21 LeuLeuLeuGlnIleGlnLysSerArgCysLeuArgAsnLeuMetLysThrProLeuPhe | Qy 32 Db 48 |
| 320 480 | 01 ThrGluAspSerAlaGlnAlaLeuIleArgGluValLeuIleLysGluLeuAlaGluGly | Qу 30 рь 42 |
| 300 420 | 81 ThrGluCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMet | Qу 28 рь 36 |
| 280 360 | 61 IleGluAlaLeuIleLysGluAsnHiSArgPheLysAsnMetValIleValThrThrThr | Qy 26 |
| 260 300 | 41 GlnargValLeuPheLeuLeuAspGlyTyrAsnGluPheLysProGlnAsnCysProGlu | Qy 24 Db 24 |
| 240 | 21 LeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLysLeuArg | Qy 22 Db 18 |
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| 180 60 | 61 LeuGlnSerProCysIleIleGluGlyGluSerGlyLysGlyLysSerThrLeuLeuGln | Qy 16 Db |
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| LeuAspLeuSerGluAsnTyrLeuGluLysAspGlyAsnGluAlaLeuHisGluLeuIle 8 | TCTGCAAATGCAGTGAAAATCCTAGCTCAGAATCTTCACAATTTTGGTCAAACTGAGCATT 8 | SerAlaAsnAlaValLysIleLeuAlaGlnAsnLeuHisAsnLeuValLysLeuSerIle | | LysSerLeuSerSerGluProCysAspLeuGluGluIleGlnLeuValSerCysCysLeu | MetCysLeuPheHisLeuThrHisLeuSerAspIleGlyGluGlyMetAspTyrIleVal | | IleLysMetAsnGluGluAspAlaIleLysLeuAlaGluGlyLeuLysAsnLeuLysLys | GlyGlyLeuThrAspSerLeuGlyAsnLeuLysAsnLeuThrLysLeuIleMetAspAsn 7 ::: | 1-089-2 (1-1024) x AX318093 (1-1395) | Innert Scores: | AX318093 AX318093 AX318093.1 GI:17900822 human. Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleos Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 Reed, J.C., Pio, F.F., Godzik, A., Stehlik, C., Damiano, J.S., Le Oliveira, V.A., Hayashi, H. and psavlowski, K. Card domain containing polypeptides, encoding nucleic acids, methods of use Patent: WO 0190156-A 98 29-NOV-2001; The Burnham Institute (US) Location/Qualifiers 1. 1395 //organism="Homo sapiens" //db_xref="taxon:9806" 277. 1356 //note="unnamed protein product" //codon_start=1 //protein_id="Call9341.1" //db_xref="GI:17900823" //translation="MNPIKONSRALIORNGMTVIKOITDDLETWNVLNREE KVEQDAARGIHMILKKGSESCNLFIKSLKEMNYFLENDGNEALHELIDRUG LIMDNIKMNEEDAIKLAGGLKNLKKMCLFHLTHLSDIGEGMDYIVKSLSSE QLVSCCLSANAYWILAQNHNLYKLSILDLSENYLEKDGNEALHELIDRUG LNLAGGNEVSSDGWLAFMGVFENLKQLVFFDESTKEFLPDPALVRKLSQVLS ARLVGWGPDDDDLSVITGAFKLVTA" 436 a 248 c 327 g 384 t | PhePheHisLysSerPheGlnGluTyrThrAlaGlyArgArgLeuSerSer 457 |
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Homo sapiens.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1395)

Damiano J. S., Stehlik, C., Pio, F., Godzik, A. and Reed, J.C.

Clan, a novel human ced-4-like gene

Genomics 75 (1-3), 77-83 (2001)
                                                                                                                                                2 (bases 1 to 1395)
Stehlik,C., Damiano,J.S., Pio,F., Godzik,A. and Reed,J.C.
Direct Submission
Submitted (21-FEB-2001) Program on Apoptosis and Cell Dea
Research, The Burnham Institute, 10901 North Torrey Pines
Jolla, CA 92037, USA
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Sequence 18:
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Command line parameters:

-MODEL-frame+_p2n.model -DEV-xlh
-C-/Ggn2_1/USPTO_Spool_VUS09697089/runat_29012003_092504_19148/app_query.fasta_1.1223
-DB-N_Geneseq_101002 -OFMT-fastap -SUFFIX-p2n.rng -MINMATCH-0.1 -LOOPCL-0
-LOOPEXT-0 -UNITS-bits -STARF-1 -END-1 -MATRIX-pam120 -TRANS-human40.cdi
-LIST-45 -DOCALIGN-200 -THR_SCORE-pot -THR_MAX-100 -THR_NIN-0 -ALIGN-15
-MODE-LOCAL -OUTFW1-pto -NORM-ext -HEAPSIZE-500 -MINLEN-0 -MAXLEN-200000000
-USER-US09697089_@CGN_1_1_344_@runat_29012003_092504_19148 -NCPU-6 -ICPU-3
-NO_MAAP -LARGEQUERY -NEG_SCORES-0 -WAIT -LONGLOG -DEV_TIMEOUT-120
-WARN_TIMEOUT-30 -THREADS-1 -XGAPOP-4 -XGAPEXT-12 -FGAPOP-6 -FGAPEXT-7
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SUMMARIES

| ; | 4.5 | 44 | 43 | 42 | 41 | 40 | 39 | 38 | 37 | 36 | 35 | 34 | 33 | 32 | 31 | 30 | 29 | 28 | 27 | 26 | 25 | 24 | 23 | 22 | 21 | 20 | 19 | 18 | 17 | 16 | 15 | 14 | | c 12 | 1 0 | 10 | oα | » ~ | ١٥ | υ | 4 | ω | 2 | | Result No. |
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| | 6133 | 6124 | 6124 | 5984 | 5984 | 5984 | 5502 | 5502 | 5366 | 5366 | 165 | 220 | 220 | 220 | 220 | 220 | 220 | 220 | 220 | 220 | 421 | 421 | 421 | 421 | 421 | 421 | 2 | 421 | 421 | 261 | 7 | 522 | 768 | 2735 | 608 | 619 | 1 2 0 E | 2950 | 2215 | 3615 | 3545 | 3396 | 3213 | 3133 | Length |
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| | Neuronal apontosis | Ovary cancer relat | Neuronal apoptosis | Human NAIP cDNA. | Human apoptosis in | Gonadotropic hormo | Neuronal apoptosis | Neuronal apoptosis | Human apoptosis in | 0 | | Human genome-deriv | #9197 ı | #17590 used | #1352 | bone m | brain e | | foetal | Human breast cell | genome-der | #4204 used | #4450 | | bone n | brain | #4236 f | foetal | breas | CDNA | cDNA | CDNA | | colon | Himan CDNA encodin | CUNA | CUNA | proce | 0 | Human caspase recr | Murine EST-derived | Human cDNA encodin | | n caspase re | Description |

ALIGNMENTS

RESULT 1 AAS03945 Human caspase recruitment domain 12 (CARD-12) cDNA. 12-SEP-2001 (first entry) AAS03945; AAS03945 standard; cDNA; 3133 ВP

Caspase recruitment domain; CARD-12; apoptosis; stress-related pathway; cancer; viral infection; poxvirus; adenovirus; autoimmune disorder; systemic lupus erythematosis; arthritis; neurological disorder; stroke; Alzheimer's disease; amyotrophic lateral sclerosis; haematologic disease; aplastic anaemia; myocardial infarction; inflammatory disorder; crohn's disease; insulin-dependent diabetes; contact dermatitis; psoriasis; graft rejection; bacterial infection; lepromatous leprosy; tuberculosis; ischaemic brain injury; hypoxic brain injury; ss;

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Alignment
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                                                                                                         US-09-697-089-2 (1-1024)
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                                                                                                                                                                                                                         The sequence represents a cDNA which encodes the human caspase CC recruitment domain 12 (CARD-12) polypeptide. CARD domains are found in a CC number of proteins that transmit signals that activate apoptosis and CC number of proteins that transmit signals that activate apoptosis and CC inflammatory pathways in response to stress and other stimuli. Therefore, CC CARD-12 and its corresponding nucleic acid may be used in treatment and CC diagnosis of patients suffering from disorders associated with an CC abnormal level (an increase or a decrease) of apoptotic cell death or CC abnormal level (an increase or a decrease) of apoptotic cell death or CC cancer, viral infections (e.g. caused by poxviruses, adenoviruses), CC autoimmine disorders (e.g. systemic lupus crythematosis, arthritis), CC neurological disorders (e.g. Alzheimer's disease, amyotrophic lateral CC infarction, stroke), inflammatory and immune system disorders (e.g. CC crohn's disease, insulin-dependent diabetes, contact dermatitis, CC psoriasis, graft rejection), bacterial infections (e.g. tuberculosis, CC lepromatous leprosy), ischaemic and hypoxic brain damage, acute bacterial CC meningitis and liver disease.
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       Human; secreted polypeptide; nervous disease; muscular disease; tumour; gastrointestinal ulceration; spinal cord disease; trachea disease; thyroid gland disease; ovary disease; prostate disease; heart disease; renal gland disease; small intestine disease; thymus disease; lymph node disease; muscular system disease; colon disease; lipase deficiency; cystic fibrosis; pancreatitis; clot formation; myocardial infarction; angioplasty; liver disease; coagulation disorder microbial disease; immune disorder; inflammation; transplant rejection; bone thickness; bone density; ferroxidase loss; apoptosis; vascular smooth cell proliferation; vaccine; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence encodes a human secreted polypeptide. The secreted polypeptides and polynucleotides are useful for treating nervous and muscular diseases, for inhibiting tumour formation and metastasis, for treating gastrointestinal ulceration, for preventing and treating diseases in spinal cord, thyroid gland, ovary, prostate, renal gland, small intestine, heart, trachea, thymus, lymph node, muscular everement of the tracker of the secretary tracker.
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P-PSDB; AAG67527.
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| 340 | 1 LeuLeuGlnIleGlnLlysSerArgCysLeuArgAsnLeuMetLysThrProLeuPhe | Qу 32 | ^ |
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| 320 | hrGluAspSerAlaGlnAlaLeuIleArgGluValLeuIleLysGluLeuAlaGluGl | Οу 30 | _ |
| 1038 | 9 ACTGAGTGCCTGAGGCACATACGGCAGTTTGGTGCCCCTGACTGCTGAGGTGGGGGGATATG | Db 97 | _ |
| 300 | hrGluCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMe | Оу 28 | _ |
| 978 | 9 ATCGAAGCCCTGATAAAGGAAAACCACCGCTTCAAGAACATGGTCATCGTCACCACCTACC | Db 91 | _ |
| 280 | 1 IleGluAlaLeuIleLysGluAsnHisArgPheLysAsnMetValIleValThrThrTh | Ωу 26 | ~ |
| 918 | | Db 85 | _ |
| 260 | lnArgValLeuPheLeuLeuAspGlyTyrAsnGluPheLysProGlnAsnCysProGl | · | _ |
| 858 | 9 CTGGATATACCTGGCACAATCAGGAAGCAGACATTCATGGCCATGCTGAAGCTGCGG | Db 79 | _ |
| 240 | 1 LeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLysLeuAr | Qy 22 | _ |
| | 9 TTC | Db 73 | _ |
| 220 | 1 PhePheLeuArgLeuSerArgAlaGlnGlyGlyLeuPheGluThrLeuCysAspGlnLe | Оу 20 | _ |
| 738 | 9 CGAATTGCCATGCTCTGGGGGTCCGGAAAGTGCAAGGCTCTGACCAAGTTCAAATTGGTC | Ĭ | _ |
| 200 | 1 ArgIleAlaMetLeuTrpGlySerGlyLysCysLysAlaLeuThrLysPheLysPheV | Оу 18 | _ |
| 678 | | Db 61 | _ |
| 180 | 1 LeuGlnSerProCysIleIleGluGlyGluSerGlyLysGlyLysSerThrLeuLeuGl | у 1 | _ |
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| ת | 1 ArdIvsAspGlnHisHisHisArgValCluClnI⊕uThrIouAspGlvI⊖uIouGlnAl | _ | _ |
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| 140 | 1 GlyGluAspIleAspIleIlePheAsnLeuLysSerThrPheThrGluProValLeuTr | Ωу 12 | _ |
| 498 | 39 TIGGCTCAGGATTTAAAGGACTTGTACCATACCCCATCTTTTCTGAACTTTTATCCCCTT | Db 43 | |
| 120 | 1 LeuAlaGlnAspLeuLysAspLeuTyrHisThrProSerPheLeuAsnPheTyrProLe | Оу 10 | |
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               MetAlaSerTrpGluLysAlaAlaGluAspThrGlyGlyIleHisMetGluGluAlaPro
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cc containing polypeptide, or a CARD, NB-ARC, ANGIO-R, LRR or SAM domain CC from it, and the polynuclectides encoding them. Also included are a cc recombinant vector comprising the polynuclectide, recombinant cells containing the vector (e.g. bacteria, yeast, plant, animal, mammalian CC and insect cells) and an anti-CARD antibody. The CARD-containing cp polypeptide and CARD-encoding nucleic acid are useful for treating a CC pathology characterised by abnormal cell proliferation (e.g. cancer), cc abnormal cell death (apoptosis), autoimmune diseases or inflammation. In CC particular, the polypeptide and nucleic acid are useful for treating cc pathology the proliferation in arteries following balloon angioplasty commuscle cell proliferation in arteries following balloon angioplasty communication arthritis, lupus, Schrogen's syndrome, Crohn's disease, communication, heart failure, communication and disease, stroke, myocardial infarction, heart failure, immunication of disease, stroke, myocardial infarction, heart failure, communication of disease (e.g. Parkinson's disease or Alzheimer's communication of disease (e.g. human containing protein.
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                                                                                                                                      GATATTGACATTATTTTAACTTGAAAAGCACCTTCACAGAACCTGTCCTGTGGAGGAAG
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Query Match:
DB:
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21-JAN-2000;
25-APR-2000;
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                                                                                                                                                                                                                                                                                  anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic;
antiaggregant; haemostatic; vulnerary; antiulcer; osteopathic;
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                                                                                                                                                                                                                                                                                                                                    cancer; ulcer; HIV infection; human
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           99US-0471275.
2000US-0488725.
2000US-0552317.
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                                                                                                                                                                                                                                                                                                                                                             encoding cDNA sequence
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AAH99166 to AAH99904 encode the human proteins given in AAM2525 to Cells they are proteins can have activities based on the tissues and CC cells they are expressed in, such as: antiinflammatory; antirheumatic; cardiant; cc antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant; cc cardiovascular; antianemnic; antiaggregant; haemostatic; vulnerary; cc antiulcer; osteopathic; dermatological; antiallergic; antiasthmatic; cr antidabetic; cytostatic; neuroprotective; antidepressant; nootropic; cc antidabetic; cytostatic; neuroprotective; antidepressant; nootropic; cr antiparkinsonian; and immunostimulant. The proteins and polynucleotides encoding them can be used in gene therapy antisense therapy and vaccine cc production. The proteins and polynucleotides are useful for screening for agonists or antagonists of a protein and for the treatment and diagnosis of disorders associated with the activity of a protein e.g. inflammation, neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal infections, autoimmunity, genetic diseases, haematopoietic disorders, cancemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers, csteoporosis, severe combined immunodeficiency, eczema, allergic cr rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression, altoriars disease, Parkinson's disease, neurodegenerative and
Sequence 2950
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Score: Alignment М :. 0 3346.00 99.53% 99.38% 61.29% Length:
Matches:
Conservative:
Mismatches:
Indels:

US-09-697-089-2 (1-1024) x AAH99581 (1-2950)

Gaps:

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Percent Similarity:
Best Local Similarity:
Query Match:

- В Q 383 N 61
- δÃ 403 SerHisLysPheAspPheGluLeuGlnAspValSerSerValAsnGluAspValLeuLeu 422
- 밁 62 TCCCACAAGTTTGATTTCGAACTGCAGGATGTCCCAGCGTGAATGAGGATGTCCTGCTG 121
- 맑 δõ 122 423 ThrThrGlyLeuLeuCysLysTyrThrAlaGlnArgPheLysProLysTyrLysPhePhe ACAACTGGGCTCCTCTGTAAATATACAGCTCAAAGGTTCAAGCCAAAGTATAAATTCTTT 181 442
- В Ω 182 443 HisLysSerPheGlnGluTyrThrAlaGlyArgArgLeuSerSerLeuLeuThrSerHis CACAAGTCATTCCAGGAGTACACAGCAGGACGAAGACTCAGCAGTTTATTGACGTCTCAT 462 241
- Š 463 GluProGluGluValThrLysGlyAsnGlyTyrLeuGlnLysMetValSerIleSerAsp
- 멍 242 GAGCCAGAGGAGGTGACCAAGGGGAATGGTTACTTGCAGAAAATGGTTTCCATTTCGGAC 482 301
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       AspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGluGlnLeuThr
                                                                                        GACATTGGAGAGGGAATGGATTACATAGTCAAGTCTCTGTCAAGTGAACCCTGTGACCTT
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10-OCT-2000;
14-MAR-2001;
23-MAY-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CC containing the vector (e.g. bacteria, yeast, plant, animal, mammalian CC and insect cells) and an anti-CARD antibody. The CARD-containing CC polypeptide and CARD-encoding nucleic acid are useful for treating a CC pathology characterised by abnormal cell proliferation (e.g. cancer), CC abnormal cell death (apoptosis), autoimmune diseases or inflammation. In CC particular, the polypeptide and nucleic acid are useful for treating content of the polypeptide and nucleic acid are useful for treating content of the polypeptide and nucleic acid are useful for treating content of the polypeptide and nucleic acid are useful for treating content of the polypeptide and nucleic acid are useful for treating content of the polypeptide and nucleic acids, smooth content of the polypeptide and nucleic acids, smooth content of the proliferation in arteries following balloon angioplasty content of the proliferation, and the proliferation and the proliferation and the proliferation, heart failure, content of the proliferation as a content of the proliferation are useful content of the proliferations. The present sequence is a content of the proliferation and protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an isolated caspase recruitment domai containing polypeptide, or a CARD, NB-ARC, ANGIO-R, LRR or SA from it, and the polynucleotides encoding them. Also included recombinant vector comprising the polynucleotide, recombinant
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New caspase recruitment do encoding nucleic acids, us or cell death, autoimmune

domain (CARD)-containing polypeptides and useful for treating abnormal cell proliferation ne diseases or inflammation, e.g. carcinomas,

or,

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Alignment Scores:
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Query Match:
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The invention relates to an isolated caspase recruitment domain (CARD) containing polypeptide, or a CARD, NB-ARC, ANGIO-R, LRR or SAM domain from it, and the polypucleotides encoding them. Also included are a recombinant vector comprising the polypucleotide, recombinant cells

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RESULT 10
ABK22767
ID ABK22767
AC ABK22
XX Caspa
KW Autoi
KW Infla
KW Dallo
KW Icuka
KW Dallo
KW WO200
XX Parxi
KW Myocaa
PR 11-00
PR 110-00
PR 110-00
PR 110-00
PR 24-MA
PR 23-MA
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23-MAY-2001;
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Oliveira
                                                                                                        New caspase recruitment domain (CARD)-containing polypeptides encoding nucleic acids, useful for treating abnormal cell prolor cell death, autoimmune diseases or inflammation, e.g. carci
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VAM, Hayashi H, P
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2000US-0225213

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diagnosing, used as foo nucleic acid molecules encoding 461 human secreted proteins for gnosing, preventing, treating or ameliorating medical conditions d as food additives or preservatives and

Claim SEQ ID No 339; 980pp; English.

CC The invention relates to isolated nucleic acid molecules and their CC encoded secreted proteins. The nucleic acids and proteins are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, cc prevent, treat or ameliorate a medical condition in e.g. humans, mice, cc rabbits, goats, horses, cats, dogs, chickens or sheep. They cc are also used in diagnosing a pathological condition or susceptibility to a pathological condition. Antibodies to the proteins can also be used in alleviating symptoms associated with the disorders and in cc diagnostic immunoassays e.g. radioimmunoassays or enzyme linked include autoimmune diseases e.g. rheumatoid arthritis, cardiovascular disorders e.g. rheumatoid arthritis, cardiovascular disorders e.g. rheumatoid arthritis, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, or and disorders e.g. cardiac arrest pathological fungional conditions caused by bacteria, viruses and funging conditions caused by bacteria, viruses and funging conditions and many other conditions caused by bacteria viruses and funging conditions and many other also be used to aid wound healing and epithelial cell proliferation, to convert skin aging due to sunburn, to maintain organs before converted the condition of primary tissues, to the conditions are considered to the properties, to the conditions are considered to the properties, to the conditions are considered to the properties, to the conditions are conditions and the conditions are conditions and the conditions are conditions. regenerate tissues and in chemotaxis. The polypeptides can also be as a food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors and other nutritional components. The present sequence encodes a novel secreted ng due to sunburn, to maintain organs before for supporting cell culture of primary tissues, to as and in chemotaxis. The polypeptides can also be used protein of the invention.

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Percent Similarity:
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 9.63e-140
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AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon cancer-associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The co
                                                                                                                     Nucleic acids encoding 4277 human useful for preventing, diagnosing
                                                                                                                                                                                                                                                                                                                                  29-SEP-1999;
03-NOV-1999;
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and/or treating colorectal cancers -
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CC cancer antigens have cytostatic activity and can be used in gene CC therapy and vaccine production. N and P may be used in the prevention, CC diagnosis and treatment of diseases associated with inappropriate P CC expression. For example, N and P may be used to treat disorders CC in a patient's genome that affect the activity of P by expressing CC inactive proteins or to supplement the patients own production of P. CC Additionally, N may be used to produce the colon cancer-associated Ps, CC inscrive proteins or to supplement the patients own production, diagnosis CC in the proteins. N and P can be used in the prevention, diagnosis CC and treatment of colorectal carcinomas and cancers. AAH37194 to AAH37204 CC and AAB77789 represent sequences used in the exemplification of the CC present invention.

CC N.B. Pages 666 to 682 and page 7053 of the sequence listing were CC missing at time of publication, meaning no sequences are present for CC SEQ ID NO:1027 to 1052, 7921 and 7922.
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26-MAR-2002

(first

entry)

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Query
DB:
                                                                                                                                                 Percent Similarity:
Best Local Similarity:
   us-09-697-089-2
                                                                                                                                                                                     The invention relates to an isolated caspase recruitment domain (CARD)
C containing polypeptide, or a CARD, NB-ARC, ANGIO-R, LRR or SAM domain
CC from it, and the polynucleotides encoding them. Also included are a
CC recombinant vector comprising the polynucleotide, recombinant cells
CC containing the vector (e.g. bacteria, yeast, plant, animal, mammalian
CC and insect cells) and an anti-CARD antibody. The CARD-containing
CC ophypeptide and CARD-encoding nucleic acid are useful for treating a
CC pathology characterised by abnormal cell proliferation (e.g. cancer),
CC abnormal cell death (apoptosis), autolimune diseases or inflammation. In
CC particular, the polypeptide and nucleic acid are useful for treating
CC (restenosis), gliomas, carcinomas, sarcomas, melanomas, leukaemias,
CC (allergies, arthritis, lupus, Schrogen's syndrome, Crohn's disease,
CC allergies, arthritis, lupus, Schrogen's syndrome, Crohn's disease,
CC neurodegenerative disease, stroke, myocardial infarction, heart failure,
CC inmunodeficiency virus (HIV) infection). The nucleic acids are useful
CC in a variety of diagnostic applications. The present sequence is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             abnormal cell proliferation; CARD; SS; NB-ARC; ANGIO-R; LRR; SAM; autoimmune disease; inflammation; cancer; abnormal cell death; apoptosis; inflammatory hyperplasia; fibrosis; smooth muscle cell proliferation; balloon angioplasty; restenosis; glioma; carcinoma; sarcoma; melanoma; leukaemia; allergy; arthritis; lupus; Schrogen's syndrome; Crohn's disease; graft-versus-host disease; stroke; myocardial infarction; heart failure; neurodegenerative disease; Parkinson's disease; Alzheimer's disease; HIV; human immunodeficiency virus infection.
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14-MAR-2001;
23-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New caspase recruitment domain (CARD)-containing polypeptides and encoding nucleic acids, useful for treating abnormal cell proliferation or cell death, autoImmune diseases or inflammation, e.g. carcinomas, arthritis or stroke
                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 178-179;
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31-JAN-2000;
04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
11-MAR-2000;
18-APR-2000;
19-MAY-2000;
07-JUN-2000;
28-JUN-2000;
30-JUN-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hyperproliferative disorder; cardiovascular disorder; cardiac cerebrovascular disorder; cerebral ischaemia; angiogenesis; nervous system disorder; Alzheimer's disease; infection; ocula corneal infection; wound healing; epithelial cell proliferatios skin ageing; food additive; preservative; antiproliferative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; opthalmalogical; vulnerary; secreted protein; rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human cDNA encoding a novel secreted
                                                                                                                                                                                                                                                                                                             17-JAN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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2000US-0179065.
2000US-0180628.
2000US-0184664.
2000US-0186350.
2000US-0189874.
2000US-019076.
2000US-0198123.
2000US-0298123.
2000US-0205515.
2000US-0209467.
2000US-0215135.
2000US-0215135.
2000US-0216647.
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2000US-0216880. 2000US-0217487. 2000US-0217496. 2000US-0218290. 2000US-0220963.

2000US-0220964.
2000US-0224519.
2000US-0224513.
2000US-0225214.
2000US-0225267.
2000US-0225267.
2000US-0225268.
2000US-0225279.
2000US-0225279.
2000US-0225447.
2000US-02251757.
2000US-02251758.
2000US-02251758.
2000US-02251758.

2000US-0226681. 2000US-0226868. 2000US-0227182. 2000US-0227009.

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20-OCT 2000
21-OCT 2000
01-NOV 2000
08-NOV 2000
017-NOV 2000
17-NOV 2000
17-NO
           The invention relates to isolated nucleic acid molecules and their encoded secreted proteins. The nucleic acids and proteins are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a pathological condition. Antibodies to the proteins can also be used in alleviating symptoms associated with the disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme linked
                                                                                                                                                                                                           New nucleic acid molecules encoding 461\ human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions used as food additives or preservatives -
                                                                                                                                                                               Claim
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P-PSDB; AAU16588.
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enzyme linked
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2000US-022994.
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2000US-02304.
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2000US-0235.
2000US-0239.
2000US-0241785.
2000US-0241785.
2000US-0241785.
2000US-0241786.

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DB:
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              Human cDNA encoding CLAN C
                                            26-MAR-2002
                                                                         ABK22733;
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                                                                                                                                                                  GTGCGGCAGAGGGTTCTTTCNTCTTG
                                                                                                                                                                                                                                                                                                      eValPhe-PheLeuArgLeuSerArgAlaGlnGly-GlyLeuPheGluThrLeuCysAsp
                                                                                                                                                                                                                                                                                                                                                                   GlnArgIleAlaMetLeuTrpGlySerGlyLysCysLysAlaLeuThrLysPheLys-Ph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTTGGTGAAGATATTGACATTATTTTTAACTTGAAAAGCACCTTCACAGAACCTGTCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AspLeuAlaGlnAspLeuLysAspLeuTyrHisThrProSerPheLeuAsnPheTyrPro
                                                                                                                                                                                                                             CAATTCCG-GGTATACCGGGACA-TTCAGGAGGCAGACATTCAGGCCNGGT---GCTGAG
                                                                                                                                                                                                                                                       GlnLeuLeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLys
                                                                                                                                                                                                                                                                                        CGTCTTCTTTCCTCCTGTTCAGCAGGGCCCCAGGGTGGGACTTTTTGAAACCCTCTGTGAT
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                                                                                                      standard;
                                            (first entry)
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725.00
89.47%
87.72%
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Alignment : Pred. No.:
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                         The invention relates to an isolated caspase recruitment domain (CARD) C -containing polypeptide, or a CARD, NB-ARC, ANGIO-R, LIRR or SAM domain CC from it, and the polynucleotides encoding them. Also included are a cC recombinant vector comprising the polynucleotide, recombinant cells C containing the vector (e.g. bacteria, yeast, plant, animal mammalian CC and insect cells) and an anti-CARD antibody. The CARD-containing CC polypeptide and CARD-encoding nucleic acid are useful for treating a CC polypeptide and carbised by abnormal cell proliferation (e.g. cancer), CC abnormal cell death (apoptosis), autoimmune diseases or inflammation. In CC particular, the polypeptide and nucleic acid are useful for treating CC keratinocyte hyperplasia, inflammatory hyperplasia, fibrosis, smooth CC muscle cell proliferation in arteries following balloon angioplasty CC (restenosis), gliomas, carcinomas, sarcomas, melanomas, leukaemias, CC allergies, arthritis, lupus, Schrogen's syndrome, Crohn's disease, CC allergies, arthritis, lupus, Schrogen's syndrome, Crohn's disease, CC disease) or immunodeficiency stroke, myocardial infarction, heart failure, CC immunodeficiency virus (HIV) infection). The nucleic acids are useful CC in a variety of diagnostic applications. The present sequence is a CC cDNA encoding a CARD domain containing protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-OCT-2000;
14-MAR-2001;
23-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New caspase recruitment domain (CARD)-containing polypeptides and encoding nucleic acids, useful for treating abnormal cell proliferation or cell death, autoimmune diseases or inflammation, e.g. carcinomas, arthritis or stroke
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 177;
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| Sear Job 1 | Оβ | Qy | Д | Qγ | В | Qy | Db | Qy | В |
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| ch con | 517 | 81 | 457 | 61 | 397 | 41 | 337 | 21 | 277 |
| Search completed: January 31, 2003, 08:55:35 Job time : 532 secs | 517 TTTCAGGACTTGAATGGACAAAGTCTT 543 | PheGlnAspLeuAsnGlyGlnSerLeu 89 | AAGGGTTCAGAGTCCTGTAACCTCTTTCTTAAATCCCCTTAAGGAGTGGAACTATCCTCTA 516 | 61 LysGlySerGluSerCysAsnLeuPheLeuLysSerLeuLysGluTrpAsnTyrProLeu 80 | 397 ATTTGCTGCGAGAAGGTGGAGCAGGATGCTGCTAGAGGGATCATTCACATGATTTTGAAA 456 | 41 IleCysCysGluLysValGluGlnAspAlaAlaArgGlyIleIleHisMetIleLeuLys 60 | AAGCAAATCACAGATGACCTATTTGTATGGAATGTTCTGAATCGCGAAGAAGTAAACATC 396 | 21 LysGlnIleThrAspAspLeuPheValTrpAsnValLeuAsnArgGluGluValAsnIle 40 | |

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GenCore version 5.1.3
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| Database : EST:* 1 | Command line parameters: -MODEL-frame+ p2n.model -DEV-xlh -MODEL-frame+ p2n.model -DEV-xlh -Q-(cgn2_1/USDT0_spoo1/USD9697089/runat_29012003_092505_19166/app_query.fasta_1.1223 -Q-(cgn2_1/USDT0_spoo1/USD9697089/runat_29012003_092505_19166/app_query.fasta_1.1223 -DE-EST -OFMT-fastap -SUFFIX-p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS-bits -START=1 -END=-1 -MATRIX=pam120 -TRANS-human40.cdi -LIST=45 -DOCALIGN-200 -THR_SCORE-pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT-pto -NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -USER-USD9697089_GCN1_1_1_2475_@runat_29012003_092505_19166 -NCPU=6 -ICPU=3 -NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=4 -XGAPDEXT=12 -FGAPOP=6 -FGAPEXT=7 -YGAPOP=4 -YGAPEXT=12 -DELOP=6 -DELEXT=7 | Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries | Minimum DB seq length: 0 Maximum DB seq length: 2000000000 | mber of hits satisfying chosen par | Scoring table: PAM120 Xgapop 4.0, Xgapext 12.0 Ygapop 4.0, Ygapext 12.0 Fgapop 6.0, Fgapext 7.0 Delop 6.0, Delext 7.0 Searched: 16154066 segs, 8097743376 residues | Title: US-09-697-089-2 Perfect score: 5459 Sequence: 1 MNFIKDNSRALIQRMGMTVIWQFDDDDLSVITGAFKLVTA 1024 | 08:44:56 ; ; (w 50: | Copyright (c) 1993 - 2003 Compugen Ltd. OM protein - nucleic search, using frame_plus_p2n model |
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| 9 9 AI02379 5 14 BQ3658 8 17 AZ7621 9 17 AZ4846 5 13 BG9948 2 17 AZ8052 6 13 BG9943 | 3.0 499 9 AIO23 2.4 515 14 BQ365 2.3 668 17 AZ765 2.2 429 17 AZ484 2.2 345 13 BG999 | 3.0 499 9 AI0237 2.4 515 14 BQ365 2.3 668 17 AZ762 | 3.0 499 9 AIO237 2.4 515 14 BQ365 | TOTAL | 3.1 6/5 TO BBIU85 | 3.2 625 17 AZ61413 | 3.3 412 14 н25984 | 3.5 728 17 AZ72 | 3.8 5// L3 BJ03/40 | 4.0 714 9 AL657756 | 4.1 840 12 BF20784 | 4.2 509 10 AW41882 | 4.6 251 12 BF90366 | 4.8 219 17 AO28388 | 5.6 553 17 | 6.1 404 17 AQ88916 | 7.1 637 9 AL782121 | 7.3 261 10 AW33791 | 8.9 4/6 12 | 9.2 728 9 AL652549 | 9.6 637 9 AL639997 | 10.0 719 | 10.7 371 10 AV65631 | 11.2 364 9 AI26 | 11.5 //5 13 BIG | 11.8 619 17 BH | 13.5 518 17 вн | 15.1 602 17 AZ3 | 15.1 748 13 BIS | 15.3 480 10 AV | 15.6 741 13 BIE | 16.0 650 10 BB | 18.2 6 17.8 | Query Score Match Length DB ID |
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ALIGNMENTS

| REFERENCE AUTHORS | | ORGANISM | SOURCE | KEYWORDS | VERSION | ACCESSION | | DEFINITION | LOCUS | BH293386 | RESULT 1 |
|--|---|-------------------|-------------|----------|------------------------|-----------|----------------------------|--|--|----------|----------|
| Rattus. 1 (bases 1 to 697) Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., Geer,K., Shvartsbeyn | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; | Rattus norvegicus | Norway rat. | GSS. | BH293386.1 GI:17205794 | вн293386 | CH230-44G15, DNA sequence. | CH230-44G15.TV CHORI-230 Segment 1 Rattus norvegicus genomic clone | BH293386 697 bp DNA linear GSS 30-NOV-2001 | | |

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Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
Clones may be purchased from arring informmation.htm). BAC end
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Rat BAC End Sequences from Library CHORI-230 EcoRI segment Unpublished (1999)
Other_GSSs: CH230-44G15.TJ
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page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
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/note="Vector: prarbac2.1; Site_1: EcoRI; Site_2: ECHORI-330 Rat (BM/SSNHsd/MCW) BAC library produced Pieter de Jong"
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GSS.
                                                                                                                                                                                                                                                                            http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: M13-21
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                 Email: hbe@tigr.org
Clones are availabe
                                                                                                                                                                                                                                                                                                                                                           9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1998)
Other_GSSs: CITBI-E1-2528J13.TR
Contact: Shaying Zhao, William Nies
Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Adams, M.D., Rounsley, S.D., Zha
Berry, K., Granger, D., Suh, E.,
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                                                                                                                       /Glone_lib="CITBI-E1"
/Sex="male"
/Sex="male"
/Geil_type="sperm"
/Geil_type="sperm"
/note="Vector: pBeloBAC11; Site_1: EcoRI; Site_2: EcoRI;
CalTech Human BAC Library D"
a 121 c 130 g 157 t
                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="2528J13"
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E., Wible,C., Shizuya,H.,
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Sequence-Ready Simon, M. and Golden, K Hominidae;

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BB627584 BB627584.1 GI:16465218
                                                                                                                                               Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M., and Hayashizaki, Y.
                                       Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-
                                                                                                      RIKEN Mouse ESTs (Arakawa,T., Unpublished (2001)
Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                         Mus musculus
              Tel: 81-45-503-9222 Fax: 81-45-503-9216
                                                                                       Laboratory for Genome Exploration Research Group, RIKEN
                                                                                                                                                                                                                                                                                                                          house mouse.
                                                                                                                                                                                                                                                          nmalia; Eutheria; (bases 1 to 650)
genome-res@gsc.riken.go.jp.
                                                                                                                                    (Arakawa, T., et al. 2001)
                                            230-0045,
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ValGluGlnLeuThrLeuAsnGlyLeuLeuGlnAlaLeuGlnSerProCysIleIleGlu 168

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                                                                                                                                             Query Match:
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AATCTGGAGAAAACCTTCACAGAACCTATCATGTGGAAGAAGGACCATCGTCATCACCGT
                       AsnLeuLysSerThrPheThrGluProValLeuTrpArgLysAspGlnHisHisHisArg 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) KOndo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizaw,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for
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Y. and Hayashizaki,Y.
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/note="Site_1: Sa
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/dev_stage="adult"
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/db_xref="taxon:10090"
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| GGTTACAATGAATTCCATCCCCAGAACTGCCCAGAAATTGAAGCCCTGATAAAGGAAAAC
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                                                                                       NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Ir
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Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:5179909"
/clone=1ib="NIH_MGC_115"
/lab_host="DH10B"
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Eukaryota; Metazoa; (
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1 (bases 1 to 480)
Qian,B., Wu,T., Huang
, Xu,X., Li,N., Peng,

Chordata;
Primates;

Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.

Huang,Q., Huang,C., Kang,B.,
Peng,Y., Liu,F., Qu,J., Song.

Song, H.,

Cheng, Z.,

Zeng,L.,

Gao, X.,

Xu, Z.,

Xiao, ÌH. Homo sapiens human.

AV719179 AV719179 GLC AV719179 AV719179.1 EST.

GI:10816331 Homo

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sapiens

cDNA clone

mRNA

RNA linear GLCEQA10 5',

mRNA sequence.

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Percent Similarity:
Best Local Similarity:
Query Match:
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              leIleCysCysGluLysValGluGlnAspAlaAlaArgGlyIleIleHisMetIleLeuL
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AAGCTCTCCAGAG-CCCTGCATCATTGAAGGG
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Conservative:
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                                                                          GATGATGATCTCAGTGTTATTACAGGAGCTTTTAAACTAGTAACTGCT
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Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park,
201203, P. R. China
Tel: 86-21-50801519(ex.45)
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603066455F1 NIH_MGC_118
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Homo sapiens cDNA GLC clones
Unpublished (2000)
mRNA sequence
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clone is available at CHGC
Location/Qualifiers
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/dev_stage="Adult"
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High quality sequence stop: 744.
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM11541 row: m_column: 14
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Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies,
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National Institutes of Health,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5215669"
/clone_lib="NIH_MGC_118"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Invitrogen). Research Genetics tracking code 027. Note:
this is a NIH_MGC Library."
148 c 166 g 198 t
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/lab_host="DH10B"
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|TIGGCTCAGGATTTACAAAGGACTTGTACCATACCCCATCTTTTCTGAACTTTTATCCCC
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                                                                                                                                                                                                                                                                                                                                                                                              Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0103 row: H column: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert B. University of Utah University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dunn, D., Aoyagi, A., Bar
Islam, H., Longacre, S.,
                                                                                                                                                                                                                                                                                                                                     Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
Class: plasmid ends
Location/Qualifiers
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Mammalia; |
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m,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and
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                                                                                                                                                                                         /sex-Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                               /organism="Mus musculus"
/strain="057BL/63"
/db_xref="ftaxon:10090"
/clone="UUGC1M0103H11"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
                                                                                                                                                               Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/).
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purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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US-09-697-089-2 (1-1024) x AZ360053
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                                                                                                                                             518 bp CH230-42F7.TV CHORI-230 Segment CH230-42F7, DNA sequence. BH348417
1 (bases 1 to 518)
Zhao,S., Shetty,J.,
,A., Gebregeorgis,E.
                                                                                    Rattus norvegicus
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                                           Rattus
                                                                      Eukaryota;
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                                                       Chordata;
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                                              AGGAACTTCAGGTGATTTTGTCAGGAGCCTAGACTACTGTGGAGACCTGGCCCTGGAAGG
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Clones are derived from the rat BAC library CHORI-230
(Attp://www.chori.org/Dacpac/rat230.htm). For BAC library
(Attp://www.chori.org/Dacpac/rat230.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.or
Clones may be purchased from BACPAC Resources
(Attp://www.chori.org/Dacpac/or ering_information.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
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Class: BAC ends.
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Fax: 301 838 0208
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CH230-19B22, DNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, Tel: 301 838 0200 Fax: 301 838 0208
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Other_GSSs: CH230-19B22.TV
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Rat BAC End Sequences from Library CHORI-230 EcoRI segment
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                      Tissue Procurement: Lothar Hennighausen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               house mouse
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Clone distribution: MGC clone distribution information
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/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Priscilla Furth, NIH Reference for transgenic model: Li et al., Cell Growt and Differentiation 7, 3-11 (1996)."
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           Contact: Shaying Zhao
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
The Institute for Genomic Research
                                                                                                                                                                                                                                                                     BH358172
CH230-18E7.TJB CHORI-230
CH230-18E7, DNA sequence.
BH358172
                                                                    Jong,P. and Fraser,C.M.
Rat BAC End Sequences from
Unpublished (1999)
Other_GSSs: CH230-18E7.TVB
                                                                                                                Zhao,S., Shetty,J., Sha,A., Gebregeorgis,E., C
Jong,P. and Fraser,C.M.
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    Medical Center
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Rodentia;
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., Overton, L., Russell, D.,
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RESULT 12
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Best Local Similarity:
Query Match:
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AI263294
qx57b01.x1 NCI_CGAP_Pan1
mRNA sequence.
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Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.or
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/or ering_information.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
plate: 18 row: E column: 7
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Class: BAC ends.
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/note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: E
/note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: E
/note="Vector: Rat (BN/SsNHsd/MCW) BAC library produced
PIETER de Jong"
182 c 199 g 225 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /strain="BN/SsNHsd/MCW"
/db_xref="taxon:10116"
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RESULT 13
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                                             LeuSerLysLeuThrPheLeuGlnGluAlaArgLeuValGlyTrpGlnPheAspAspAsp 1010
                                                                                                                                                                           GACTTTAGTACTAAAGAATTTCTACCTGATCCAGCATTAGTCAGAAAACTTAGCCAAGTG
                                                                                                                                                                                            AspPheSerThrLysGluPheLeuProAspProAlaLeuValArgLysLeuSerGlnVal 990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Life Technologies catalog #: 11548-013
DNA Sequencing by: Washington University Genome Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 2146 Std Error: 0.00
Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, I
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 364)
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National Cancer Institute, Cancer Genome Anat
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84 c 55 g 108 t
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/tissue_type="adenocarcinoma"
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/db_xref="taxon:9606"
/clone="IMAGE:2005417"
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                                                                      SerLeuValLeuSerThrCysLysAsnIleTyrSerLeuMetValGluAlaSerProLeu 724
                                                                                                                                            SerSerAlaThrSerLeuArgLeuGlnIleLysArgCysAlaGlyValAlaGlySerLeu 704
                                                                                                                                                                                                                  ThrLeuArgAspPheSerLysLeuAsnLysGlnAspIleThrTyrLeuGlyLysIlePhe 684
                                                                                                                                                                                                                                                                                        ProSerArgAlaValSerLeuPhePheAsnTrpLysGlnGluPheArgThrLeuGluVal
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                                                                                                                         AGCTCTGCCACAAGCCTCAGGCTGCAAATAAAGAGATGTGCTGGTGGCTGGAAGCCTC
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AV656315 GLC :
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Hu,G., Gu,J., Chen,Z. and Han,Z.
Insight into hepatocellular carcingenesis at transcriptome level
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: hanzg@chgc.sh.cn
This clone is available at CHGC
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chinese National Human Gen 351 Guo Shoujing Road, Zha 201203, P. R. China Tel: 86-21-50801919(ex.45)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
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/db_xref="taxon:9606"
/clone="GLCEQA10"
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/dev_stage="Adult"
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1 to 371)
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Zhangjiang Hi-Tech Park, Pudong, Shanghai
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Best Local Similarity:
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UI-R-DN1-cmv-e-08-0-UI.S1 UI-R-DN1 Rattus
UI-R-DN1-cmv-e-08-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to verify it as a clone from the normalized distal colon library cDNA Library Preparation: M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com) The following repetitive elements were found in this cDNA sequence: 12-210, >LIPB3#LINE/LI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            451 Eckstein Medical Research Building Iowa City, IA 52242, USA Tel: 319 335 8250
Fax: 319 335 9565
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University of Iowa
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Eukaryota; Metazoa;
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                                                                                                                                                                                                                                                                                                                                /lab_host="DHIOB (Life Technologies)"
/lab_host="DHIOB (Life Technologies)"
/note="vector: pT73D-Pac (Pharmacia) with a modified
/note="vector: pt753D-Pac (Pharmacia) with a modified
/note="vector: pt753D-Pac (Pharmacia) with a modified
polylinker; Site_1: Rot 1; Eco RI; The UI-R-DNI
library is a normalized Rat Distal Colon library (nRDC)
constructed in pT3T7 PAC vector according to the procedure
described by Bonaldo, Lennon & Soares (Normalization and
Subtraction: Two Approaches to Facilitate Gene Discovery.
Genome Research 6: 791-806, 1996). The oligonucleotide
used to prime first strand synthesis contained the
sequence tag GAAGTGCTCC between the Not I cloning site and
DT18 stretch. The Rat Distal Colon tissue was provided by
Tom Freeman of the Sanger Center.
                                                                                                                                                                                                                                                           TAG_SEQ-GAAGTGCTCC"
                                                                                                                                                                                                                                                                                     TAG_LIB=UI-R-DN1
TAG_TISSUE=distal colon
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/clone_lib="UI-R-DN1"
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/db_xref="taxon:10116"
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Silurana tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                 Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2
TROPICALIS_SEQUENCE_ID: TNeu003d13.sp6
                                                                                                                                                                                                                                                                                                                   Contact: Huckle E
Sanger Centre
                                                                                                                                                                                                                                                                                                                                                Huckle, E., Taylor, R., Ashurst, J.L., 2orn, A.M. and R
Sanger Xenopus tropicalis EST project 2001 (10_2001
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mRNA sequence.
AL639997
AL639997.1 GI:16792128
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AL639997 XGC-neurula
                                                                                                                                                                                                       This sequence is from a Xenopus Gene Collection constructed by Aaron M. Zorn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EST
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   ۵
/clone_lib="XGC-neurula"
/dev_stage="neurula"
/dev_stage="neurula"
/lab_host="Escherichia coli DH10B"
/note="Vector: pCS107; Site_1: EcoRI; Site_2: Not
was oligo dr primed from 5ug of poly A+ RNA from
was oligo dr primed from 5ug of poly A+ RNA from
EcoRI-NotI cut cDNA was then ligated into pCS107
EcoRI at the 5' end and NotI at the 3' end."
3 c 132 g 185 t 1 others
                                                                                                                                                                                                                                                                                                   Cambridgeshire, CB10 1SA,
                                                                                                                            /organism="Silurana tropicalis"
/db_xref="taxon:8364"
/clone="TNeu003d13"
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TNeu003d13 5',
                                                               NotI; cDNA
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ATCTCCAACATTGGAGAGTGGCATGGAGAGTGTTGCCAT
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-DB-Issued_Patents_NA -OEMT-fastap -SUFFIX-p2n.rni -MINMATCH-0.1 -LOOPCL-0
-LOOPEXT-0 -UNITS-bits -START= .EDD-1 -TH-P2n.rni -MINMATCH-0.1 -LOOPCL-0
-LOOPEXT-0 -UNITS-bits -START= .EDD-1 -TH-P2n.rni -MINMATCH-0.1 -LIGN-15
-LIST-45 -DOCALIGN-200 -THR_SCORE-PCt -THR_MAX=100 -THR_MIN-0 -ALIGN-15
-MODE-LOCAL -OUTFMT-Pto -NORM-ext -HEAPSIZE-500 -MINLEN-0 -MAXLEN-2000000000
-USER-US09697089_@CGN_1_1_46.@runat_29012003_092505_19177 -NCPU-6 -ICPU-3
-NO_MARN_TIMEOUT-30 -THREADS-1 -XGAPOD-4 -XGAPEXT-12 -FGAPOD-6 -FGAPEXT-7
-YGAPOP-4 -YGAPEXT-12 -DELOP-6 -DELEXT-7
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US-09-353-585-1

US-08-910-731-5

US-08-824-701A-8

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| 1, 1 | Sequence 17, Appl | ٦, | 'n | 4. | 4, | e 13, | e 13, | Sequence 13, Appl | 13, | e 13, | ب | 7, | 7, | e 7, | e 1, | e 1, | e 1, | 1, | 'n | Ø | 42, | e 42, | e 44, | Sequence 2, Appli | e 1, | e 7, | equence 7, | equence | equence 25, | equence 2 | e 25, | Sequence 9, Appli |

ALIGNMENTS

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                                 US-09-697-089-2 (1-1024) x US-08-836-134-1 (1-5502)
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                                                                                                                                                                                                                                                   SEQ ID NO 1
LENGTH: 5502
TYPE: DNA
                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Neuronal Apoptosis Inhibitor Protein, Gene Sequence Patent No. 6020127

TITLE OF INVENTION: Mutations Causative of Spinal Muscular Atrophy FILE REFERENCE: 3477-112, 033477/139914

CURRENT APPLICATION NUMBER: US/08/836,134A

CURRENT FILING DATE: 1997-06-20

NUMBER OF SEQ ID NOS: 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Roy, Natalie APPLICANT: Ikeda, Joh-e
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                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Ver. 2.0
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                             TGTAAGCGCCTACAACAATTTTTTGAACTATGTCTCCAGCCTCCCTTCAACAAAAGCAGG
                                                                                         GCAGGAACATCAAGATTTGGGACTGTATCATTTGAAACAAATCAACTCACCCATGATGAC
                                                                                                                   uProGluGluValThrLysGlyAsnGlyTyrLeuGlnLysMetValSerIleSerAspIl
                                                                                                                                                 TCCTGCCTTCCAAGAATTTCTTGCGGGGATGAGGCTGATTGAACTCCTGGATTCAGATAG
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                                                                                                                                                                                                                                                                                    sPheAspPheGluLeuGlnAspVal-----SerSerValAsnGluAspValLeuLeuTh 423
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TITLE OF INVENTION: Neuronal Apoptosis Inhibitor Protein, Gene Sequence
Patent No. 6429011
TITLE OF INVENTION: Mutations Causative of Spinal Muscular Atrophy
FILE REFERENCE: 3477-112, 033477/139914
CURRENT APPLICATION UNMEER: US/09/493,784
CURRENT FILING DATE: 2000-01-28
PRIOR APPLICATION UNMEER: 08/836,134
PRIOR APPLICATION UNMEER: 08/836,134
PRIOR FILING DATE: 1997-06-20
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PatentIn Ver. 2.0
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APPLICANT: Korneluk, Rober
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Mahadevan, Mani S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2223 ATATTACGGAAGCTCTTTTCACATAATATGACTCGTCTGCGAAAGTTTATGGTTTACTTT
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                                                                        ZIP: 22201-4714

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTIN RELEASE #1.0, Vers

CURRENT APPLICATION NUMBER: US/09/353,585

FILING DATE: 15-Jul-1999

CLASSIFICATION: C12N 15/29, 15/82, A0
  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/930,277
FILING DATE: 27-OCT-1997
                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon & Vanderhye PC
STREET: 8th Floor, 1100 No. 6287865th
                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Plant pathogen thereof
                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Dixon, Mark S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rThrGlyLeuLeuCysLysTyrThrAlaGlnArgPheLysProLysTyrLysPhePheHi 443
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                                                                                                                                                                                                                                                 CITY: Arlington
STATE: Virginia
COUNTRY: United States of America
ZIP: 22201-4714
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Jones, Jonathan DG
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Query Match:
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                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/09353585 Patent No. 6287865 GENERAL INFORMATION:
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TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 3573 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                   1154
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                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                  NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESSE: Nixon & Vanderhye PC
STREET: 8th Floor, 1100 No. 6287865th Glebe Road
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FILING DATE: 01-APR-1996
APPLICATION NUMBER: GB 9506658.5
FILING DATE: 31-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: MS MATY J W11SOD
REGISTRATION NUMBER: 32,955
                                                                                                                                                                                                                TITLE OF INVENTION: Plant pathogen resistance genes and uses thereof
                                                                                                                                                                                                                                                                       APPLICANT: Dixon, Mark S
Jones, David A
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                                                                                                                                                                                                                                                                                                                                                                                                                               TTGTATCTTTACAAT 1168
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                                                      CITY: Arlington
STATE: Virginia
COUNTRY: United States
ZIP: 22201-4714
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STRANDEDNESS: double
                                                                                                                                                                                                                                                       Jones, Jonathan DG
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95.00
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  IBM PC
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compatible
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Matches:
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alignment Scores:
              Sequence 5, Application US/08910731 Patent No. 5932440 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEO ID NO: 1:
                                                                                                                                                                                                                                                           2721
 APPLICANT:
                                                                                                                   2838 TIGTATCTTTACAAT 2852
                                                                                                                                                                                     2781 AACCAGCTTTCTGGCTCTATTCCTGCTTCATTGGGGAAT---CTGAACAACTTGTCTATG
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                                                                                                                                                   793 MetCysLeuPheHis 797
                                                                                                                                                                                                                                                                       753 GlyGlyLeuThrAspSerLeuGlyAsnLeuLysAsnLeuThrLysLeuIleMetAspAsn 772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORIGINAL SOURCE:
ORGANISM: Tomato
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NAME: MS MATY J Wilson
REGISTRATION NUMBER: 3:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
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LENGTH: 6471 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: (703) 816-4000
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                                                                                                                                                                                                                                                     IleLysMetAsnGluGluAspAlaIleLysLeuAlaGluGlyLeuLysAsnLeuLysLys 792
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SOFTWARE:
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FILING DATE: 15-U11-1999
CLASSIFICATION: C12N 15/29, 15/82, A01H 5/00, A01N 65/00, C12Q
1/68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: sig_peptide LOCATION: 1677...1753
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FILING DATE: 01-APR-1996
APPLICATION NUMBER: GB 9506658.5
FILING DATE: 31-MAR-1995
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CHATTERJEE, DEB K.
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36.92%
1.74%
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Matches:
Conservative:
Mismatches:
Indels:
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Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: US-08-910-731-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 202-371-2540 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: SHANDILYA, HARINI
TITLE OF INVENTION: Mammalian Ribonuclease Inhibitors and Use Thereof
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/024,057 FILING DATE: 16-AUG-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 08/7
FILING DATE: 03-FEB-1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/795,395
FILING DATE: 04-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
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                                                                                                                 867
                                                                                                                                                         334
                                                                                                                                                                                                847
                                                                                                                                                                                                                                                          827 LeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeuAlaGlnAsnLeuHisAsn 846
454
                                                                              394
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                                                                                                                                                                                                                                                                                                                  214 GGCGTGCATTGCGTGCTCCAGGGCCTGCAGACCCCCTCCTGCAAGATCCAGAAGCTGAGC 273
                                                                                                                                                                                                                                                                                                                                                     807 GlyMetAspTyrIleValLysSerLeuSerSerGluProCysAspLeuGluGluIleGln 826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 202 371-2540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: ESMOND, ROBERT W. REGISTRATION NUMBER: 32, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE: (Herew CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 20005-3934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH:
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                               etLeuProTrpGlyCysAspValGlnGlySer 895
                                                                                                             AlaLeuHisGlu---LeuIleAspArgMetAsnValLeuGluGlnLeu--ThrAlaLeuM 885
                                                                            CTGCTCTGCGAAGGACTCCTGGACCCCCAGTGCCGCCTGGAAAAGCTGCAGCTGGAGTAT 453
                                                                                                                                                                               LeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeuGluLysAspGlyAsnGlu 866
TGCAGCCTCTCGGCTGCCAGCTGCGAGCCCCT
                                                                                                                                                         CTGCCCACCCTGCAGGAGCTGCACCTCAGCGACAACCTCTTGGGGGGATGCGGGCCTGCAG
                                                                                                                                                                                                                                 CTCCAGAACTGCTGACGGGGCCGGCCGGGGTCCTCCAGCACACTACGCACC 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T: 1100 NEW YORK AVE., N.W., SUITE 600
WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nucleic acid
EDNESS: both
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29.35%
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RESULT 7
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Query Match:
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Best Local Similarity:
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US-08-824-701A-8
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Sequence 2, Application US/09228986 Patent No. 6359198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 8, Application US/08824701A Patent No. 5882868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (302) 798-0700
TELEFAX: (302) 798-5970
INFORMATION FOR SEQ ID NO: 8:
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LENGTH: 250 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/824,701A
FILING DATE: 14-APR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lew, Jeffrey C.
REGISTRATION NUMBER: 35935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Diskette 3.5 inch, 1.44 Mb storage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 47
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Method of Diagnosing Spinal Muscular Atrophy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Funanage, Vici
APPLICANT: Scavina, Mena
                                                                                        179
                                                                                                                                                                                                                                                                                                                                     218 AspGlnLeuLeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeu
                                                                                                                 278 ThrThrThrGluCysLeuArgHisIleArgGlnPhe 290
                                                                                                                                                                                                                                                                238 LysLeuArgGlnArgValLeuPheLeuLeuAspGlyTyrAsnGluPheLysProGlnAsn 257
                                                                                                                                                            122 ---CAAGTCATAGGAAAACTGATTCAAAAAACCACTTATCCCGGACCTGCCTATTGATT 178
                                                                                                                                                                                              258 CysProGluIleGluAlaLeuIleLysGluAsnHisArgPheLysAsnMetValIleVal 277
                                                                                                                                                                                                                                  62 CAGTTAAAGAATCAGGTCTTATTCCTTTTAGATGACTACAAAGAAATATGTTCAATCCCT 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                       2 GACCAGCTCCTAGAGAAAGAAGGATCTGTTACTGAAATGTGCATGAGGAACATTATCCAG 61
                                                                                      GCTGTCCGTACAAACAGGGCCAGGGACATCCGCCGATAC
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82.00
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31.51%
1.50%
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WS-09-041A-27
; Sequence 27, Application US/09099041A
; Patent No. 6340576
; Patent INFORMATION:
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; TYPE: DNA
; ORGANISM: Euci
US-09-228-986-2
                                                                                                          Percent Similarity:
Best Local Similarity:
Query Match:
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                                                    US-09-697-089-2 (1-1024) x US-09-099-041A-27 (1-1470)
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                                                                                                                                                                                                                                                                  ; SEQ ID NO 27
; LENGTH: 1470
; TYPE: DNA
; ORGANISM: HOMO S
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CURRENT FILING DATE: 1999-01-12
NUMBER OF SEQ ID NOS: 130
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Bertin, John
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
FILE REFERENCE: 07334-076001
CURRENT APPLICATION NUMBER: US/09/099,041A
CURRENT FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 09/019,942
PRIOR FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Strabala, Timothy APPLICANT: Nieuwenhuizen, Niels
                                                                                                                                                                                                                                                                                                                                                SOFTWARE:
156 GlyLeuLeuGlnAlaLeuGlnSerProCysIleIleGluGlyGluSerGlyLysGlyLys 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            628 AATCGCCTCTTTGGCTCGATTCCCATGAAGATAGCCGAT 666
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        753 GlyGlyLeuThrAspSerLeuGlyAsnLeuLysAsnLeuThrLysLeuIleMetAspAsn 772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              508 ACAAAGCTGGGATCTCTGAAGAAGCTCAGTGTTCTTGCTCTGCAATCTAATCAGCTCACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  733 ThrSerValThrAsnLeuLysThrLeuSerIleHisAspLeuGlnAsnGlnArgLeuPro 752
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Matches:
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448 GGCATCCTCAATGAGCAGGGTGAGACCATCTTCATCCTGGGTGATGCTGGGGTGGGCAAG

1470 20 7

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507

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Sequence 27, Application US/09207359B

Patent No. 6469140

GENERAL INFORMATION:

APPLICANT: Bertin, John
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
CURRENT FILING DATE: 1934-11201

CURRENT APPLICATION NUMBER: US/09/207,359B

CURRENT FILING DATE: 1998-12-08

PRIOR APPLICATION NUMBER: US 09/099,041

PRIOR FILING DATE: 1998-06-17

PRIOR FILING DATE: 1998-02-06

NUMBER OF SEQ ID NOS: 47

SOFTWARE: FASTSEQ for Windows Version 4.0
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US-09-207-359B-27
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DB:
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CURRENT FILING DATE: 1999-02-05
EARLIER APPLICATION NUMBER: US 09/207,359
EARLIER FILING DATE: 1998-12-08
EARLIER APPLICATION NUMBER: US 09/099,041
EARLIER FILING DATE: 1998-06-17
EARLIER APPLICATION NUMBER: US 09/019,942
EARLIER FILING DATE: 1998-02-06
NUMBER FILING DATE: 1998-02-06
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SOFTWARE: FastSEQ for Windows Version 4.0
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ORGANISM: Homo sapiens
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                       US-09-245-281-9
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APPLICANT: Bertin, John
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
FILE REFERENCE: 07334-076001
CURRENT APPLICATION NUMBER: US/09/09,041A
CURRENT FILING DATE: 1998-06-17
     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 9
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PRIOR FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 37
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TYPE: DNA
ORGANISM: Homo
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ORGANISM: Homo sapiens
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   9, Application US/09245281
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GENERAL INFORMATION:

APPLICANT: Bertin, John

TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED

TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF

ETILE REFERENCE: 07334-112001

CURRENT APPLICATION NUMBER: US/09/207,359B

CURRENT FILING DATE: 1998-12-08

PRIOR APPLICATION NUMBER: US 09/099,041

PRIOR APPLICATION NUMBER: US 09/099,041

PRIOR APPLICATION NUMBER: US 09/019,942

PRIOR FILING DATE: 1998-02-06

NUMBER OF SEO ID NOS: 47

SOFTWARE: FastSEQ for Windows Version 4.0
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EARLIER FILING DATE: 1998-12-08
EARLIER APPLICATION NUMBER: US 09/099,041
EARLIER FILING DATE: 1998-06-17
EARLIER APPLICATION NUMBER: US 09/019,942
EARLIER FILING DATE: 1998-02-06
EARLIER FILING DATE: 1998-02-06
NUMBER OF SEO ID NOS: 44
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TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 07334/118001
CURRENT APPLICATION NUMBER: US/09/245,281
CURRENT FILING DATE: 1999-02-05
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TYPE: DNA
ORGANISM: Homo
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TYPE: DNA
ORGANISM: Homo sapiens
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US-09-245-281-25
US-09-245-281-25
Sequence 25, Application US/09245281
Patent No. 6369196
GENERAL INFORMATION:
APPLICANT: Bertin, John
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 07334/118001
CURRENT APPLICATION NUMBER: US/09/245,281
CURRENT FILING DATE: 1999-02-05
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Best Local Similarity:
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US-09-099-041A-25
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LENGTH: 3080
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APPLICANT: Bertin, John
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CURRENT FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 09/019,942
PRIOR FILING DATE: 1998-02-06
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SOFTWARE: FastSEQ for Windows Version
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Matches:
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EARLIER APPLICATION NUMBER: US 09/207,359
EARLIER FILING DATE: 1998-12-08
EARLIER APPLICATION NUMBER: US 09/099,041
EARLIER FILING DATE: 1998-06-17
EARLIER APPLICATION NUMBER: US 09/019,942
EARLIER FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 44
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 25
LENGTH: 3080
TYPE: DNA
ORGANISM: Homo Sapiens
US-09-245-281-25
                                                                                                                                                                                                                                                                      Percent Similarity:
Best Local Similarity:
Query Match:
Search completed: January 31, 2003, 10:46:23 Job time: 106 secs
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Pred. No.:
Score:
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                                                                                                             448 GGCATCCTCAATGAGCAGGGTGAGACCATCTTCATCCTGGGTGATGCTGGGGTGGGCAAG 507
                                                       |||||| ||| ||| 568 AAATTCTTCTTCCACTTT 585
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Command line parameters:

-MODEL-frame+_p2n.model -DEV-xlh
-MODEL-frame+_p2n.model -DEV-xlh
-O_-Cgn2_1/USPTO_Spool_VG09697089/runat_29012003_092506_19222/app_query.fasta_1.1223
-DB-Published_Applications_NA -QFMT-fastap -SUFFIX-p2n.rnpb -MINNATCH-0.1
-LOOPEXT-0 -UNITS-blts -START=1 -END--1 -MATRIX-ppam120
-TRANS-human40.cdi -LIST-45 -DOCALIGN-200 -THR_SCORE-pct -THR_MAX=100
-THR_MIN-0 -ALIGN-15 -MODE-LOCAL -OUTFMT-pto -NORM-ext -HEAPSIZE-500 -MINLEN-0
-MAXLEN-200000000 -USER-US09697089_@CGN_1_1_60_erunat_29012003_092506_19222
-NCPU-6 -ICPU-3 -NO_XLPXY -NO_MMAP -LARGEQUERY -NOE_SCORES-0 -WAIT -LONGLOG
-DEV_TIMEOUT-120 -WARN_TIMEOUT-30 -THREADS-1 -XGAPEXT-12 -FGAPOP-6
-FGAPEXT-7 -YGAPOP-4 -YGAPEXT-12 -DELOP-6 -DELEXT-7
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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/cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
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  Sequence 3,
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ALIGNMENTS

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RESULT 1
US-09-841-739-3
                     Percent Similarity:
Best Local Similarity:
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  Query Match:
                                                                Score:
                                                                                                       Alignment Scores:
                                                                                                                                               US-09-841-739-3
                                                                                   Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Bertin, John
                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THE FILE REFERENCE: 07334-329001
CURRENT APPLICATION NUMBER: US/09/841,739
CURRENT FILING DATE: 2001-08-29
PRIOR APPLICATION NUMBER: US 09/697,089
PRIOR APPLICATION NUMBER: US 09/697,089
PRIOR APPLICATION NUMBER: US 09/61,822
PRIOR FILING DATE: 2000-10-26
PRIOR FILING DATE: 1999-10-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/09841739 Patent No. US20020034784A1
                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                  SOFTWARE: FastSEQ
                                                                                                                                                          TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                  for Windows Version 4.0
5459.00
100.00%
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100.00%
                                                              Length:
Matches:
                     Conservative: Mismatches:
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DB:

10

Gaps:

| | 360 | $341\ \ ValValIle Thr Cys \texttt{AlaIleGlnMetGlyGluSerGluPheHisSerHisThrGlnThr}$ | Qy |
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| . <u> </u> | 1020 | | Db |
| | 340 | ${\tt uLeuLeuGlnIleGlnLysSerArgCysLeuArgAsnLeuMetLysThrPro}$ | Qy |
| ַנַם | | 901 ACAGAAGACAGCGCCCAGGCTCTCATCCGAGAAGTGCTGATCAAGGAGCTTGCTGAAGGC | 망 |
| | 320 | ${\tt luAspSerAlaGlnAlaLeuIleArgGluValLeuIleLysGluLeuAlaGluGluAleuAlaGluGluGluAleuAlaGluGluGluAleuAlaGluGluGluAleuAlaGluGluGluAleuAlaGluGluGluGluAleuAlaGluGluGluGluGluGluGluGluGluGluGluGluGluG$ | Qy |
| D D | 300 | 281 ThrGluCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMet | Qy |
| | 840 | 81 ATCGAAGCCCTGATAAAGGAAAACCACCGCTTCAAGAACATGGTCATCGTCA | Ď |
| <u> </u> | 280 | 6 | Qy |
| 2 5 | 780 | 721 CAGAGGGTTCTTTTCCTTCATGATGGCTACAATGAATTCAAGCCCCAGAACTGCCCAGAA | Db |
| g | 260 | 241 GlnArgValLeuPheLeuLeuAspGlyTyrAsnGluPheLysProGlnAsnCysProGlu | Qy |
| · • • | 240 720 | 221 LeuaspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLysLeuArg | Фр |
| 2 5 | 660 | 601 TTCTTCCTCCGTCTCAGCAGGGCCCAGGGTGGACTTTTTGAAACCCTCTGTGATCAACTC | 망 |
| 2 5 | 220 | 201 PhePheLeuArgLeuSerArgAlaGlnGlyGlyLeuPheGluThrLeuCysAspGlnLeu | Qy |
| | 600 | 541 CGCATTGCCATGCTCTGGGGCTCCGGAAAGTGCAAGGCTCTGACCAAGTTCAAATTCGTC | рb |
| | 200 | 181 ArgIleAlaMetLeuTrpGlySerGlyLysCysLysAlaLeuThrLysPheLysPheVal | Qy |
| | 180 | 161 LeuGlnSerProCysIleIleGluGlyGluSerGlyLysGlyLysSerThrLeuLeuGln | Оy |
| 9 5 | 480 | | Дb |
| 2 19 | 160 | rgLysAspGlnHisHisHisArgValGluGlnLeuThrLeuAsnGlyLeuLeuGlnAla | Qy |
| , p | 420 | | Db |
| .9 | 140 | luaspIleAspIleIlePheAsnLeuLysSerThrPheThrGluProValLeuTrp | Qy |
| ַ טַ | 120 360 | 101 LeuAlaGlnAspLeuLysAspLeuTyrHisThrProSerPheLeuAsnPheTyrProLeu | ОУ |
| | 300 | 241 TTTCAGGACTTGAATGGACAAAGTCTTTTTCATCAGACATCAGAAGGAGACTTTGGACGAT | Db |
| | 100 | lnAspLeuAsnGlyGlnSerLeuPheHisGlnThrSerGluGlyAspLeuAspAsp | Qy |
| <u>ם</u> | | 1 AAGGGTTCAGAGTCCTGTAACCTCTTACATCCCTTAAGGAGTGGAACTATCCTCTA | Db . |
| 9 | 80 | 1 LysGlySerGluSerCysAsnLeuPheLeuLysSerLeuLysGluTrpAsnTyrProLeu | Qy |
| <u> </u> | 60 180 | 41 IleCysCysGluLysValGluGlnAspAlaAlaArgGlyIleIleHisMetIleLeuLys | Db Qq |
| ? 5 | 120 | | Db |
| | 40 | sGlnIleThrAspAspLeuPheValTrpAsnValLeuAsnArgGluGluValAsnIle | Qy |
| ַּנִם | 20 | 1 MetasnPheIleLysaspasnSerArgAlaLeuIleGlnArgMetGlyMetThrValIle | Qy |
| 9 5 | | 9-697-089-2 (1-1024) x US-09-841-739-3 (1-3072) | us-09 |
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| 1021 GTGGCCACACACACACACACACACACACACACACACACAC | _ | | | | | | | | | | | | | | | | | | | | | | | | | _ | _ | _ | _ | | _ |
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| GuenheHisth-PhetyraspLeuLeuileGlnLysAsnLysHisLysGly 380 | | 04 | | | 92 | - ⊙ | | 1801 | 601 | 74 | 0 00 | · · | | 541 | | | 1501 | n i≱ | 4 4 | سن | 6 | ίω | 4 | 2 | 2 | 2 | 0 | 1141 | 8 | 081 | 21 |
| | LaGlySerLeuSerLeuValLeuSerThrCysLysAsnIleTyrSerLeuMetValGlu 7 | GGAAAATATTCAGCTCTGCCACAAGCCTCAGGCTGCAAATAAAAGAGATGTGCTGGTGTG | lyLysIlePheSerSerAlaThrSerLeuArgLeuGlnIleLysArgCysAlaGlyVal 7 | hrLeuGluValThrLeuArgAspPheSerLysLeuAsnLysGlnAspIleThrTyrLeu 6 | AAACCTACATTCCCAGCAGGCCTGTATCTTTGTTCTTCAACTGGAAGCAGGAATTCAGG | TGGCTTCATGGGAAAAGGCTGCAGAAGACACAGGTGGAATCCACATGGAAGAGGCCCCA 1 | etAlaSerTrpGluLysAlaAlaGluAspThrGlyGlyIleHisMetGluGluAlaPro 6 | ATTTGCCCAATTGTGCAAGTGCTCTGGACTTCATTAAACTGGACTTTTATGGGGGAGCT 1 | isLeuProAsnCysAlaSerAlaLeuAspPheIleLysLeuAspPheTyrGlyGlyAla 6 | IYAYSSETAUTYTILEASISETGIYASILLEPTOASPIYTAUHARASPPAEHEGIU | atarcaagkagracarccaaatcagccctgagccaagaarttgaagctrictricaa I | uTyrGlnGluSerThrSerLysSerAlaLeuSerGlnGluPheGluAlaPhePheGln 5 | GAGCAAGAAATTCTGAAAGCCATAAACATCAATTCCTTTGTAGAGTGTGGCCATCCAT | GluGlnGluIleLeuLysAlaileAsnIleAsnSerPheValGluCysGlyIleHis 5 | TTCCATCGCCAAGAGGCCTCTCTGGAGACAGGAATCTTTGCAAAAGTGTGAAAAACACAC | uSerIleAlaLvsArgProLenTrpArgGlnGlnSerLenGlnSerValLvsAsnThr 5 | | | erAspIleThrSerThrTyrSerSerLeuLeuArgTyrThrCysGlySerSerValGlu 5 | CTCATGAGCCAGAGGGGACCAAGGGGAATGGTTACTTGCAGAAAATGGTTTCCATT 1 | erHisGluProGluGluValThrLysGlyAsnGlyTyrLeuGlnLysMetValSerIle 4 | TCTTTCACAAGTCATTCCAGGAGTACACAGCAGGACGAAGACTCAGCAGTTTATTGACG 1 | hePheHisLysSerPheGlnGluTyrThrAlaGlyArgArgLeuSerSerLeuLeuThr 4 | GCTGACAACTGGGCTCCTCTGTAAATATACAGCTCAAAGGTTCAAGCCCAAAGTATAAA 1 | uLeuThrThrGlyLeuLeuCysLysTyrThrAlaGlnArgPheLysProLysTyrLys 4 | TGTTCTCCCACAAGTTTGATTTCGAACTGCAGGATGTGTCCAGCGTGAATGAGGATGTC 1 | alpheSerHisLysPheAspPheGluLeuGlnAspValSerSerValAsnGluAspVal 4 | GGCTGCAAGTGACTTCATTCGGAGCCTGGGACCACTGTGGAGACCTAGCTCTGGAGGGT 1 | lAlaAlaSerAspPheIleArgSerLeuAspHisCysGlyAspLeuAlaLeuGluGly 4 | Leurnen still rietyk aspledileut leotiilysasiilysats lysats lysoty | |
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RESULT 2
US-09-841-739-1
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; Patent No. US20020034784A1
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APPLICANT: Bertin, John TITLE OF INVENTION: NOV
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                                                                                                                          GlnLeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTrpLeuAlaPheMetGlyVal
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TYPE: DNA
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LeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLysLeuArg
                      PhePheLeuArgLeuSerArgAlaGlnGlyGlyLeuPheGluThrLeuCysAspGlnLeu
                                                     ArgIleAlaMetLeuTrpGlySerGlyLysCysLysAlaLeuThrLysPheLysPheVal
                                                                                                          LysGlnIleThrAspAspLeuPheValTrpAsnValLeuAsnArgGluGluValAsnIle
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| GlnLeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTrpLeuAlaPheMetGlyVal 9 | AspThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPheGln 9 | LysHisLeuGluGluValProGlnLeuValLysLeuGlyLeuLysAsnTrpArgLeuThr 9 | LeuThralaLeuMetLeuProTrpGlyCysAspValGlnGlySerLeuSerSerLeuLeu 9 | GluLysaspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGluGlu 8 | AlaGlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeu 8 | AspLeuGluGluIleGlnLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeu 8 | LeuSerAspIleGlyGluGlyMetAspTyrIleValLysSerLeuSerSerGluProCys 8 | IleLysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHis 8 | ASDLeuLySASDLeuThrLySLeuIleMetASPASDIIeLySMetASDGUGIuASPALa 7 | LeuSerIleHisAspLeuGlnAsnGlnArgLeuProGlyGlyLeuThrAspSerLeuGly 7 | AlaSerProLeuThrIleGluAspGluArgHisIleThrSerValThrAsnLeuLysThr 7 | AlaGlySerLeuSerLeuValLeuSerThrCysLysAsnIleTyrSerLeuMetValGlu 7 | GlyLysIlePheSerSerAlaThrSerLeuArgLeuGlnIleLysArgCysAlaGlyVal 7 | ThrLeuGluValThrLeuArgAspPheSerLysLeuAsnLysGlnAspIleThrTyrLeu 6 | GluThrTyrIleProSerArgAlaValSerLeuPhePheAsnTrpLysGlnGluPheArg 6 | MetAlaSerTrpGluLysAlaAlaGluAspThrGlyGlyIleHisMetGluGluAlaPro 6 | HisLeuProAsnCysAlaSerAlaLeuAspPheIleLysLeuAspPheTyrGlyGlyAla 6 | GGTAAAAGCTTATATATCAACTCAGGGAACATCCCCGATTACTTATTTGACTTCTTTGAA 1 |
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APPLICANT: Reed, John C.

APPLICANT: Bod, Frederick F.

APPLICANT: Godzik, Adam

APPLICANT: Stehlik, Christian

APPLICANT: Stehlik, Christian

APPLICANT: Lee, Sug-Hyung

APPLICANT: Lee, Sug-Hyung

APPLICANT: Hayashi, Hideki

APPLICANT: Hayashi, Hideki

APPLICANT: Hayashi, Hideki

APPLICANT: Pawlowski, Krzysztof

TITLE OF INVENTION: No. US20020176853A1el Card Domain Control of Invention: Polypeptides, Encoding Nucleic Acids

FILE REFERENCE: P-LJ 4752

CURRENT APPLICATION NUMBER: US/09/864,921

CURRENT FILING DATE: 2001-05-23

PRIOR APPLICATION NUMBER: US 09/579,240

PRIOR FILING DATE: 2000-05-24

PRIOR FILING DATE: 2000-10-10

PRIOR APPLICATION NUMBER: US 60/275,980

PRIOR FILING DATE: 2001-03-14

NUMBER OF SEQ ID NOS: 195

SOPTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 96

LENGTH: 3396
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APPLICANT: Plo, Frederick F.
APPLICANT: Godzik, Adam
APPLICANT: Stehlik, Christian
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APPLICANT: BETTIN, John
ITTLE OF INVENTION: NOVEL MOLECULES OF THE C
FILE REFERENCE: 07334-329001
CURRENT APPLICATION UNMER: US/09/841,739
CURRENT FILING DATE: 2001-08-29
PRIOR APPLICATION NUMBER: US 09/697,089
PRIOR APPLICATION NUMBER: US 60/161,822
PRIOR APPLICATION NUMBER: US 60/161,822
PRIOR APPLICATION NUMBER: US 60/161,822
PRIOR FILING DATE: 1999-10-27
NUMBER OF SEQ ID NOS: 16
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 3612
TYPE: DNA
ORGANISM: Homo sapiens
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| Qy 283 CysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMetThrGlu 302 | Oy 263 AlaLeuIleLysGluAsnH1sArgPheLysAsnMetValIleValThrThrThrThrGlu 282 | Qy 243 ValLeuPheLeuLeuAspGlyTyrAsnGluPheLysProGlnAsnCysProGluIleGlu 262 | Qy 223 IleProGlyThrIleArgLySGlnThrPheMetAlaMetLeuLeuLySLeuArgGlnArg 242 | Oy 203 LeuArgLeuSerArgAlaGlnGlyGlyLeuPheGluThrLeuCysAspGlnLeuLeuAsp 222 | Qy 183 AlaMetLeuTrpGlySerGlyLysCysLysAlaLeuThrLysPheLysPheValPhePhe 202 | Qy 163 SerProCysIleIleGluGlyGluSerGlyLysGlyLysSerThrLeuLeuGlnArgIle 182 | Qy 143 AspGlnHisHisHisArgValGluGlnLeuThrLeuAsnGlyLeuLeuGlnAlaLeuGln 162 | Qy 123 ASPIleASPIleIlePheASnLeuLySSerThrPheThrGluProValLeuTrpArgLys 142 | Qy 103 GlnaspLeuLysAspLeuTyrHisThrProSerPheLeuAsnPheTyrProLeuGlyGlu 122 | Oy 89LeuPheHisGlnThrSerGluGlyAspLeuAspAspLeuAla 102 | Qy 81 PheGlnAspLeuAsnGlyGlnSer | Qy 61 LysGlySerGluSerCysAsnLeuPheLeuLysSerLeuLysGluTrpAsnTyrProLeu 80 | Oy 41 IleCysCysGluLysValGluGlnAspAlaAlaArgGlyIleIleHisMetIleLeuLys 60 | Qy 21 LysGlnIleThrAspAspLeuPheValTrpAsnValLeuAsnArgGluGluValAsnIle 40 | Qy 1 MetAsnPheIleLysAspAsnSerArgAlaLeuIleGlnArgMetGlyMetThrValIle 20 :::: | -841-739-6 (1-3612) | nt Similarity: 98.16% Local Similarity: 98.07% Match: 95.04% | Length: Matches: |
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| 2398 TACATTCCCAG | 38 | | | 2158 CAAGAGAGTAC | | 2038 ATCGCCAAGAC | | 1918 ATTACATCCAC | | 0 — m | 1738 ACAACTGGGC | 403 SERHISLYSPI 1678 TCCCACAAGT | 383 AlaSerAspH | | 343 IleThrCysA. 1498 ATCACTTGTGG | | 1378 GACAGCGCCC 323 LeuGlnIleG | 1318 TGCCTGAGGC |

| 643 TyrIleProSerArgAlaValSerLeuPhePheAsnTrpLysGlnGlu |
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| 623 SerTrpGluLysalaAlaGluAspThrGlyGlyIleHisMetGluGluA |
| 603 ProAsnCysAlaSerAlaLeuAspPheIleLysLeuAspPheTyrGlyG |
| 583 SerLeuTyrIleAsnSerGlyAsnIleProAspTyrLeuPheAspPhePh |
| 563 GInGluSerThrSerLysSerAlaLeuSerGlnGluPheGluAlaPhePh |
| 543 GlnGluIleLeuLysAlaIleAsnIleAsnSerPheValGluCysGlyIl |
| 523 IleAlaLysArgProLeuTrpArgGlnGluSerLeuGlnSerValLysAs |
| 503 ArgAlaValMetLysHisLeuAlaAlaValTyrGlnHisGlyCysLeuLe |
| 483 IleThrSerThrTyrSerSerLeuLeuArgTyrThrCysGlySerSerVa |
| 463 GluProGluGluValThrLysGlyAsnGlyTyrLeuGlnLysMetValSer |
| 443 HisLysSerPheGlnGluTyrThrAlaGlyArgArgLeuSerSerLeuLe |
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| 403 SerHisLysPheAspPheGluLeuGlnAspValSerSerValAsnGluAs |
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| 363 PheHisThrPheTyrAspLeuLeuIleGlnLysAsnLysHisLysHisLys |
| 343 IleThrCysAlaIleGlnMetGlyGluSerGluPheHisSerHisThrG |
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SOFTWARE: FastSEQ for Wir
SEQ ID NO 4
LENGTH: 3615
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/841,73
CURRENT FILING DATE: 2001-08-29
PRIOR APPLICATION NUMBER: US 09/697,089
PRIOR FILING DATE: 2000-10-26
PRIOR APPLICATION NUMBER: US 60/161,822
PRIOR FILING DATE: 1999-10-27
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ORGANISM: Homo
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                                                                                                                                                                                                            GACCAACACCATCACCGCGTGGAGCAGCTGACCCTGAATGGCCTCCTGCAGGCTCTTCAG
                                                                      GATATTGACATTATTTTAACTTGAAAAGCACCTTCACAGAACCTGTCCTGTGGAGGAAG
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| Qy 523 IleAlaLysArgProLeuTrpArgGlnGluSerLeuG |
|---|
| Qy 503 ArgAlaValMetLysHis |
| Qy 483 IleThrSerThrTyrSerSerLeuLeuArgTyrThrCysGlyS |
| Qy 463 GluProGluGluValThrI Db 1858 GAGCCAGAGGAGGTGACCA |
| Qy 443 HistysSerPheGlnGluTyrThrAlaGlyArgArgLeuSerSerLeuLe |
| Qy 423 ThrThrGlyLeuLeuCysl |
| Qy 403 SerHisLysPheAspPhe(|
| Qy 383 AlaSerAspPheIleArgSerI |
| Qy 363 PheHisThrPheTyrAspLeuLeuIleGln |
| 343 IleThrCysAlaIleGlnMetGlyGluSerGl |
| Qy 323 LeuGlnileGlnLysSerArgCysLeuArg |
| Oy 303 AspSerAlaGlnAlaLeu |
| Qy 283 CysLeuArgHisIleArd |
| Qy 263 AlaLeuIleLysGluAsnHis |
| Oy 243 ValLeuPheLeuLeuAs |
| Qy 223 IleProGlyThrIleArd |
| Qy 203 LeuArgLeuSerArgAl |
| Qy 183 AlaMetLeuTrpGlySerGlyLys |
| Db 958 AGCCCCTGCATCATTGAAGG |

| Qy | 43 | GlnGluIleLeuLysAlaIleAsnIleAsnSerPheValGluCysGlyIleHisLeuTyr | 62 |
|------|------|---|-----|
| Db | 2098 | AAATTCTGAAAGCCATAAACATCAATTCCTTTGTAGAGTGTGGCATCCATTTATAT 2 | 157 |
| YO Y | 56 | ı G | 82 |
| 5 | Ú | AAGAGATACATCCAAATCAGCCCTGAGCCAAGAATTTGAAGCTTTCTTT | |
| Qy | 583 | SerLeuTyrIleAsnSerGlyAsnIleProAspTyrLeuPheAspPhePheGluHisLeu 6 | 02 |
| Db | 2218 | GCTTATATATATCAACTCAGGGAACATCCCCGATTACTTATTTGACTTCTTTGAACATTTG | 277 |
| ОУ | 603 | aMetAla 6 | 22 |
| 망 | 2278 | TTGTGCAAGTGCCCTGGACTTCATTAAACTGGACTTTTATGGGGGAGCTATGGCT 2 | 337 |
| Qy | 623 | pThrGlyGlyIleHisMetGluGluAlaProGluThr 6 | 42 |
| Db | 2338 | CATGGGAAAAGGCTGCAGAAGACACAGGTGGAATCCACATGGAAGAGGCCCCAGAAACC 2 | 397 |
| Qy | 643 | yrIleProSerArgAlaValSerLeuPhePheAsnTrpLysGlnGluPheArgThr | 52 |
| DЬ | 2398 | TTCCCAGCAGGGCTGTATCTTTGTTCTTCAACTGGAAGCAGGAATTCAGGACTCT | 157 |
| Qy | ω | alThrLeuArgAspPheSerLysLeuAsnLysGlnAspIleThrTyrLeuGly | 32 |
| В | 2458 | GAGGTCACACTCCGGGATTTCAGCAAGTTGAATAAGCAAGATATCAGATATCTGGGGAAA 25 | 517 |
| Qy | 683 | hrSerLeuArgLeuGlnIleLysArgCysAlaGlyValA |)2 |
| Db | 2518 | TATTCAGCTCTGCCACAAGCCTCAGGCTGCAAATAAAGAGATGTGCTGGTGTGGCTGGA 2 | 577 |
| Qy | 703 | LLeuSerThrCysLysAsnIleTyrSerLeuMetValGluAlaSer 7 | 22 |
| Dβ | 2578 | GCCTCAGTTTGGTCCTCAGCACCTGTAAGAACATTTATTCTCTCATGGTGGAAGCC | 537 |
| Qγ | 723 | ProLeuThrIleGluAspGluArgHisIleThrSerValThrAsnLeuLysThrLeuSer 74 | 2 |
| DЬ | 2638 | CCTCACCATAGAAGATGAGAGGCACATCACATCTGTAACAAACCTGAAAAACCTTG | 597 |
| Qy | 743 | IleHisAspLeuGlnAsnGlnArgLeuProGlyGlyLeuThrAspSerLeuGlyAsnLeu 76 | 2 |
| DЬ | 2698 | TTCATGACCTACAGAATCAACGGCTGCCGGGTGGTCTGACTGA | 757 |
| Qy | 763 | LysasnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluGluAspAlaIleLys 78 | 32 |
| DЪ | 2758 | AGAACCTTACAAAGCTCATAATGGATAACATAAAGATGAATGA | 317 |
| Qy | ω | LeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHisLeuSer 80 |)2 |
| ДЪ | 18 | CTGAAGGCCTGAAAAACCTGAAGAAGATGTGTTTATTTCATTTGACCCACT | 377 |
| Qy | 803 | AspIleGlyGluGlyMetAspTyrIleValLysSerLeuSerSerGluProCysAspLeu 82 | 22 |
| рь | 2878 | ACATTGGAGAGGGAATGGATTACATAGTCAAGTCTCTGTCAAGTGAACCCTGTGACCT | 337 |
| Qy | 823 | GluGluIleGlnLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeuAlaGln 84 | 12 |
| Db | 2938 | AAGAAATTCAATTAGTCTCCTGCTGCTTGTCTGCAAATGCAGTGAAAATCCTAGCTC | 997 |
| Qy | 843 | AsnLeuHisAsnLeuValLysLeuSerTleLeuAspLeuSerGluAsnTyrLeuGluLys 86 | 2 |
| Db | 2998 | ATCTTCACAATTTGGTCAAACTGAGCATTCTTGATTTATCAGAAAATTACCTGGAAAAA | 057 |
| Оу | 863 | AspGlyAsnGluAlaLeuHisGluLeuILeAspArgMetAsnValLeuGluGlnLeuThr 88 | ລັ |
| DЬ | 3058 | ATGGAAATGAAGCTCTTCATGAACTGATCGACAGGATGAACGTGCTAGAACAGCT | 17 |
| Qy | 883 | AlaLeuMetLeuProTrpGlyCysAspValGlnGlySerLeuSerSerLeuLeuLysHis 90 |)2 |
| Db | 3118 | CACTGATGCTGCCCTGGGGCTGTGACGTGCAAGGCAGCCTGAGCAGCCTGTTGAAACA | 77 |

| | 61 LysGlySerGluSerCysAsnLeuPheLeuLysSerLeuLysGluTrpAsnTyrProLeu | Qy 41 IleCysCysGluLysValGluGlnAspAlaAlaArgGlyIleIleHisMetIleLeuLys 60 | Qy 21 LysGlnIleThrAspAspLeuPheValTrpAsnValLeuAsnArgGluGluValAsnIle 40 | 1 MetAsnPheIleLysAspAsnSerArgAlaLeul ::: | 95.04% Indels: 10 Gaps: 10 Saps: 10 Gaps: 10 Gap | Pred. No.: 0 Length: 3615 Score: 5188.00 Matches: 1014 Percent Similarity: 98.16% Conservative: 1 Best Local Similarity: 98.07% Mismatches: 1 | CRGANISM: Homo sapiens US-09-841-739-12 Alignment Scores: | ; SOFTWARE: FastSEQ for Windows Version 4.0 ; SEQ ID NO 12 ; LENGTH: 3615 ; TYPE: DNA | PRIOR FILING DATE: 2000-10-26 PRIOR APPLICATION NUMBER: US 60/161,822 PRIOR FILING DATE: 1999-10-27 NUMBER OF SEQ ID NOS: 16 | | Patent NO. US20020034784A1 ; Patent NO. US20020034784A1 ; GENERAL INFORMATION: ; APPLICANT: Bertin. John ; TITLE OF INVENTION: NOVEL MOIECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE | SULT 6 -09-841-739-12/c Sequence 12. Application US/09841739 | Qy 1003 ValGlyTrpGlnPheAspAspAspAspLeuSerVallleThr 1016 | Oy 983 LeuValArgLysLeuSerGlnValLeuSerLysLeuThrPheLeuGlnGluAlaArgLeu 1002 | Qy 963 ASDIGULYSGIDLGUVALPhePheAspPheSerThrLySGIDPheLGUProAspProAla 982 | Qy 943 ASNLeuAlaGlyASNATgValSerSerAspGlyTrpLeuAlaPheMetGlyValPheGlu 962 | Qy 923 GluIleArgIleLeuGlyAlaPhePheGlyLySASnProLeuLySASnPheGlnGlnLeu 942 | Db 3178 TTGGAGGAGTCCCACAACTCGTCAAGCTTGGGTTGAAAAACTGGAGACTCACAGATACA 3237 |
|---|---|---|---|--|--|--|---|--|--|---|--|---|---|--|---|---|---|--|
| Qy 423 ThrThrGlyLeuLeuCysLysTyrThrAlaGlnArgPheLysProLysTyrLysPhePhe 442 | Qy 403 SerHisLysPheAspPheGluLeuGlnAspValSerSerValAsnGluAspValLeuLeu 422 | Qy 383 AlaSerAspPheIleArgSerLeuAspHisCysGlyAspLeuAlaLeuGluGlyValPhe 402 | | 3 IleThrCysAlaIleGlnMetGlyGluSerGluPheHisSerHisThrGlnThrThrLeu | Qy 323 LeuGlnIleGlnLysSerArgCysLeuArgAsnLeuMetLysThrProLeuPheValVal 342 | Qy 303 AspSerAlaGlnAlaLeuIleArgGluValLeuIleLysGluLeuAlaGluGlyLeuLeu 322 | Qy 283 CysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMetThrGlu 302 | Qy 263 AlaLeuIleLysGluAsnHisArgPheLysAsnMetValIleValThrThrThrThrGlu 282 | Qy 243 ValLeuPheLeuLeuAspGlyTyrAsnGluPheLysProGlnAsnCysProGluIleGlu 262 | Qy 223 IleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLysLeuArgGlnArg 242 | Qy 203 LeuArgLeuSerArgAlaGlnGlyGlyLeuPheGluThrLeuCysAspGlnLeuLeuAsp 222 | QY 183 AlaMetLeuTrpGlySerGlyLysCysLysAlaLeuThrLysPheLysPheValPhePhe 202 | Qy 163 SerProCysItelleGluGlyGluSerGlyLysGlyLysSerThrLeuLeuGlnArgile 182 | 13 ASPANIALSHISHISHISHISHISHISHISHISHISHISHISHISHIS | 123 ASPILEASPILETIEPREASILEULYSSERThEPHETHGUEPROVALLEUTEPARGLYS | 103 GINASPLeulysaspLeulystH.STRIPTOSerPnE-LeuASRPDETYFTYDLEUGLYGIU | 2898 ACCTCTTCTCTAATAGGTCTTTTTCATCAGACATCAGAAGGAGAACTTGGACGATTTGGCT | 2958 |

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APPLICANT: Reed, John C.
APPLICANT: Pio, Frederick F.
APPLICANT: Stehlik, Christian
APPLICANT: Stehlik, Christian
APPLICANT: Lee, Sug-Hyung
APPLICANT: Lee, Sug-Hyung
APPLICANT: Damiano, Jason S.
APPLICANT: Oliveira, Vasco A.
APPLICANT: Hayashi, Hideki
APPLICANT: Pawlowski, Krzysztof
APPLICANT: Pawlowski, Krzysztof
APPLICANT: Powlowski, Krzysztof
APPLICANTION: NO. US20020176853A1el Cantille OF INVENTION: No. US20020176853A1el Cantille OF INVENTION: NUMBER: US/09/664,921
CURRENT APPLICATION NUMBER: US/09/664,921
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 09/579,240
PRIOR FILING DATE: 2000-10-10
PRIOR FILING DATE: 2000-10-10
PRIOR FILING DATE: 2001-03-14
NUMBER OF SEO ID NOS: 195
SOFTWARE: FastSEQ for Windows Version 4.0
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Use

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CORMERCAL INFORMATION.

APPLICANT: Reed, John C.

APPLICANT: Godzik, Adam

APPLICANT: Stebilk, Christian

APPLICANT: Stebilk, Christian

APPLICANT: Stebilk, Christian

APPLICANT: Lee, Sug-Hyung

APPLICANT: Damiano, Jason S.

APPLICANT: Damiano, Jason S.

APPLICANT: Hayashi, Hideki

APPLICANT: Hayashi, Hideki

APPLICANT: Pawlowski, Krzysztof

TITLE OF INVENTION: Polypeptides, Encoding Nucleic Acids, and Methods of U

FILE REFERENCE: P-LJ 4752

CURRENT APPLICATION NUMBER: US/09/864,921

CURRENT FILING DATE: 2001-05-23

PRIOR APPLICATION NUMBER: US 09/579,240

PRIOR FILING DATE: 2000-05-24

PRIOR APPLICATION NUMBER: US 09/686,347

PRIOR FILING DATE: 2001-03-14

NUMBER OF SEQ ID NOS: 195

SOFTMARE: FastSEQ for Windows Version 4.0

LENGTH: 1395

TYPE: DNA

ORGANISM: Homo saplen
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Best Local Similarity:
Query Match:
DB:
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US-09-864-921-98
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TYPE: DNA
CRCANISM: Homo s
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...
US-09-864-921-181
                                                                                                                             CURRENT APPLICATION NUMBER: US/09/864,921
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 09/579,240
PRIOR ETLING DATE: 2000-05-24
PRIOR APPLICATION NUMBER: US 09/686,347
PRIOR APPLICATION NUMBER: US 09/686,347
PRIOR APPLICATION NUMBER: US 09/686,347
PRIOR APPLICATION NUMBER: US 00/275,980
PRIOR FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 195
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 181
LENGTH: 618
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APPLICANT: Oliveira, Vasco A.
APPLICANT: Hayashi, Hideki
APPLICANT: Pawlowski, Krzysztof
TITLE OF INVENTION: No. US20020176853Alel Card Domain Containing
TITLE OF INVENTION: Polypeptides, Encoding Nucleic Acids, and Methods of Use
TILE REFERENCE: P-LJ 4752
                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Reed, John C.
APPLICANT: Pio, Frederick F.
APPLICANT: Godzik, Adam
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Damiano, Jason S.
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                                                                           CURRENT APPLICATION NUMBER: US/09/764,864
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult |
NUMBER OF SEQ ID NOS: 1792
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 339
LENGTH: 608
TYPE: DNA
                                                                                                                                                                                                                         Sequence 339, Application US/09764864 Patent No. US20020132753A1 GENERAL INFORMATION:
                                                                                                                                                                                    APPLICANT: Rosen et al. TITLE OF INVENTION: Nucleic Acids, Proteins, FILE REFERENCE: PTZ23
           NAME/KEY: SITE LOCATION: (20) OTHER INFORMATION:
                                                   ORGANISM: Homo FEATURE:
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GENERAL INFORMATION:

APPLICANT: Reed, John C.

APPLICANT: Plo, Frederick F.

APPLICANT: Godzik, Adam

APPLICANT: Stehlik, Christian

APPLICANT: Damiano, Jason S.

APPLICANT: Lee, Sug-Hyung

APPLICANT: Oliveira, Vasco A.

APPLICANT: Hayashi, Hideki
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OTHER INFORMATION: |
NAME/KEY: SITE
LOCATION: (86)
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                                                                                                                                                                                                                                             GlyAlaMetAlaSerTrpGluLysAlaAlaGluAspThrGlyGlyIleHisMetGluGluIl
                                                                                                                                                                                                                                                                                      PheGluHisLeuProAsnCysAlaSerAlaLeuAspPheIleLysLeuAspPheTyrGly
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           Lee, Sug-Hyung
Oliveira, Vasco A.
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Jason S.
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; LOCATION: (277)...(744)
US-09-864-921-102
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          Sequence 754, Application | Patent No. US20020132753AI GENERAL INFORMATION: APPLICANT: Rosen et al. TITLE OF INVENTION: Nucle
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NUMBER OF SEQ ID NOS: 195
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 102
LENGTH: 768
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TITLE OF INVENTION: No. US20020176853A1el Card Domain Containing
TITLE OF INVENTION: Polypeptides, Encoding Nucleic Acids, and Methods
FILE REFERENCE: P-LJ 4752
CURRENT APPLICATION NUMBER: US/09/864,921
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 09/579,240
PRIOR FILING DATE: 2000-05-24
PRIOR FILING DATE: 2000-05-24
PRIOR FILING DATE: 2000-10-10
PRIOR APPLICATION NUMBER: US 09/686,347
PRIOR FILING DATE: 2000-10-10-10
PRIOR APPLICATION NUMBER: US 09/686,347
PRIOR FILING DATE: 2000-10-10-10
PRIOR APPLICATION NUMBER: US 60/275,980
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REFERENCE:
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; LOCATION: (505)
; OTHER INFORMATION:
US-09-764-864-754
           RESULT 13
US-09-864-921-100
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Query Match:
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Sequence
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 754
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NAME/KEY: SITE
LOCATION: (499)
OTHER INFORMATION: C
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ORGANISM: HOMO SAPIE
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NAME/KEY: SITE
LOCATION: (360)
OTHER INFORMATION: n
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CURRENT FILING DATE: 2001-01-17
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                                                                                      CAATTCCG-GGTATACCGGGACA-TTCAGGAGGCAGACATTCAGGCCNGGT---GCTGAG
                                                                                                 GlnLeuLeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLys 238
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                                                       GCTCTTCAGAGCCCCTGCATCATTGAAGGGGAATCTGGCAAAGGCAAGTCCAYTCTGCTG
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; TYPE: DNA
; ORGANISM: Homo sapi
; FEATURE:
; EAME/KEY: CDS
; LOCATION: (277)...(
US-09-864-921-100
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CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 09/579,240
PRIOR FILING DATE: 2000-05-24
PRIOR APPLICATION NUMBER: US 09/686,347
PRIOR FILING DATE: 2000-10-10
PRIOR APPLICATION NUMBER: US 60/275,980
PRIOR APPLICATION UMBER: US 60/275,980
PRIOR FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 195
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 100
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US-09-864-921-177
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APPLICANT: Pio, Frederick F.
APPLICANT: Godzik, Adam
APPLICANT: Stehlik, Christian
APPLICANT: Stehlik, Christian
APPLICANT: Damiano, Jason S.
APPLICANT: Lee, Sug-Hyung
APPLICANT: Oliveira, Vasco A.
APPLICANT: Hayashi, Hideki
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TITLE OF INVENTION: No. US20020176853Alel Card Domain Containing
TITLE OF INVENTION: Polypeptides, Encoding Nucleic Acids, and M
FILE REFERENCE: P-LJ 4752
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                                                                                                                                                                                                            GENERAL
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LENGTH: 261
                                                                                             APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/864,921
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 09/579,240
PRIOR FILING DATE: 2000-05-24
PRIOR APPLICATION NUMBER: US 09/686,347
PRIOR FILING DATE: 2000-10-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Hayashi, Hideki
APPLICANT: Pawlowski, Krzysztof
TITLE OF INVENTION: NO. US20020176853A1el Card Domain Containing
TITLE OF INVENTION: Polypeptides, Encoding Nucleic Acids, and Methods
FILE REFERENCE: P-LJ 4752
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PRIOR APPLICATION NUMBER: US 60/180,312 PRIOR FILING DATE: 2000-02-04 PRIOR APPLICATION NUMBER: US 60/207,456
                                                  CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
                                                                                     FILE REFERENCE: Aeomica-X-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/275,980 PRIOR FILING DATE: 2001-03-14 NUMBER OF SEQ ID NOS: 195 SOFTWARE: FastSEQ for Windows Version 4.0
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TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                PheGlnAspLeuAsnGlyGln
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PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
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FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00665
FILING DATE: 2001-01-30
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                         ValPhePheAspPheSerThrLysGluPheLeuProAspProAlaLeuValArgLysLeu
                                                                                GGTGCATTTTTTGGAAAGAACCCTCTGAAAAACTTCCAGCAGTTGAATTTGGCGGGAAAT
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NUMBER: US 09/608,408
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N FETAL LIVER, SIGNAL = 1.2 
IN LUNG, SIGNAL = 1.2 
IN BRAIN, SIGNAL = 1.2 
IN HEART, SIGNAL = 1.2 
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IN HELA, SIGNAL = 1.6 
IN HELA, SIGNAL = 1.8 
IN PLACENTA, SIGNAL = 1.8 
IN BI474, SIGNAL = 1.5
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Search completed: January 31, 2003, 11:43:49 Job time : 154 secs

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databases daily. The split freed up more machine time for processing searches. results. These databases were split into to two parts to reduce the time needed to update the Pending Nucleic Acid and/or Pending Amino Acid database searches now generate two sets of

extensions, .rnpm and .rnpn Searches run against the Nucleic Acid Pending database produce two sets of results, with the

extensions, .rapm and .rapn Searches run against the Amino Acid Pending database produce two sets of results, with the

contain data that is confidential. The Pending database search results should not be left in the case because they THIS PAGE BLANK (USPTO)

GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd

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-MODEL-frame+_p2n, model -DEV-xlh
-Q-/cgn21/USPTO_spool/US09697089/runat_29012003_092505_19190/app_query.fasta_1.1223
-DB-Pending_Patents_NA_Main -QFMT-fastap -SUFFIX=p2n.rnpm -MINMATCH-0.1
-DB-Pending_Patents_NA_Main -QFMT-fastap -SUFFIX=p2n.rnpm -MINMATCH-0.1
-LOOPEL-0 -LOOPEXT-0 -UNITS-blts -START-1 -END-1 -MATRIX-pam120
-TRANS-human40.cdi -LIST-45 -DCCALIGN-200 -THR_SCORE-pct -THR_MAX-100
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-MAXLEN-200000000 -USER-US0697089_@CGN_1_1_3843_@runat_29012003_092505_19190
-NCPU-6 -ICPU-3 -NO_XLPXY -NO_MMAP -LARGEDUERY -NEG_SCORES-0 -WAIT -LONGLOG
-DEV_TIMEDUT-120 -MARN_TIMEOUT-30 -THREADS-1 -XGAPEXT-12 -FGAPEXT-12 -FGAPOP-6
-FGAPEXT-7 -YGAPOP-4 -YGAPEXT-12 -DELOP-6 -DELEXT-7
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/cgn2_6/ptodata/2/pna/US06_COMB.seq:*
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4.0 , Ygapext 12.0
6.0 , Fgapext 7.0
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302 / cgnn2_6/ptodata/2/pna/US097B_COMB.seq; *
311 / cgnn2_6/ptodata/2/pna/US097B_COMB.seq; *
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313 / cgnn2_6/ptodata/2/pna/US098B_COMB.seq; *
314 / cgnn2_6/ptodata/2/pna/US099B_COMB.seq; *
315 / cgnn2_6/ptodata/2/pna/US099B_COMB.seq; *
316 / cgnn2_6/ptodata/2/pna/US099B_COMB.seq; *
317 / cgnn2_6/ptodata/2/pna/US099C_COMB.seq; *
318 / cgnn2_6/ptodata/2/pna/US099C_COMB.seq; *
319 / cgnn2_6/ptodata/2/pna/US1010B_COMB.seq; *
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422 / cgnn2_6/ptodata/2/pna/US1010B_COMB.seq; *
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467 / cgnn2_6/ptodata/2/pna/US1011_COMB.seq; *
468 / c
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIE

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| 5459 5459 5459 | |
| 100.0 100.0 100.0 100.0 | |
| 3072 3072 3072 3072 3133 3133 3133 | Length |
| 1 27 1 27 27 32 | B |
| PCT-US00-29643-3 US-09-697-089-3 US-09-841-739-3 PCT-US00-29643-1 US-09-697-089-1 US-09-841-739-1 | ID |
| Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli | Description |

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APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: MILLENNIUM PHARMACEULES OF THE C
TITLE OF INVENTION: NOVEL MOLECULES OF THE C
TITLE OF INVENTION: PROTEIN FAMILY AND USES
FILE REFERENCE: 07334-136W01
CURRENT APPLICATION NUMBER: PCT/US00/29643
CURRENT FILING DATE: 2000-10-26
PRIOR APPLICATION NUMBER: US 60/161,822
PRIOR APPLICATION NUMBER: US 60/161,822
PRIOR APPLICATION NUMBER: US 60/161,822
PRIOR FILING DATE: 1999-10-27
NUMBER OF SEG ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
                                                                                       Alignment
Pred. No.:
                                         Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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PCT-US00-29643-3
Sequence 3, Application PC/TUS0029643
Sequence 1, Application PC/TUS0029643
                       US-09-697-089-2 (1-1024) x
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LENGTH: 3072
TYPE: DNA
ORGANISM: Homo:
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4 US-09-922-279A-1319
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6 PCT-US00-29643-4
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7 US-09-697-089-1
2 US-09-697-089-1
2 US-09-697-089-1
2 US-09-697-676-911
2 US-09-577-676-917
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                                                                                                        GlyGluAspIleAspIleIlePheAsnLeuLysSerThrPheThrGluProValLeuTrp
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                              LeuLeuLeuGlnIleGlnLysSerArgCysLeuArgAsnLeuMetLysThrProLeuPhe
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                                                                      TIGITGCTCCAAATTCAGAAATCCAGGTGCTTGAGGAATCTCATGAAGACCCCTCTCTTT
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960 340 900

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| CURRENT APPI | | laSerProLeuThrIleGluAspGluArgHisIleThrSerValThrAsnLeuLysThr 740 | 721 Alas | Qy |
|--|-------|--|--|----------|
| APPLICANT: TITLE OF INT TITLE OF INT | | AlaGlySerLeuSerLeuValLeuSerThrCysLysAsnIleTyrSerLeuMetValGlu 720 | 701 Alag 2101 GCTG | Ф |
| US-09-697-089-: ; Sequence 3, i ; GENERAL INFO | , C | GlyLysIlePheScrSerAlaThrSerLeuArgLeuGlnIleLysArgCysAlaGlyVal 700 | 681 GlyL 2041 GGGA | DP QA |
| 3061 CTAG | Db | hrLeuGluValThrLeuArgAspPheSerLysLeuAsnLysGlnAspIleThrTyrLeu 680 | 661 ThrLeu 1981 ACTCTG | Qy Db |
| 001 | Db C | luThrTyrIleProSerArgAlaValSerLeuPhePheAsnTrpLysGlnGluPheArg 660 | 641 GluTh 1921 GAAAC | Оу |
| 941 | 0 D 4 | MetAlaSerTrpGluLysAlaAlaGluAspThrGlyGlyIleHisMetGluGluAlaPro 640 | 621 MetAl 1861 ATGGC | Дb |
| | מם | H15LeuProAsnCysAlaSerAlaLeuAspPheIleLysLeuAspPheTyrGlyGlyAla 620 | 601 Hist 1801 CATT | Ωу |
| u 0-0 | O D X | GlyLysSerLeuTyrIleAsnSerGlyAsnIleProAspTyrLeuPheAspPhePheGlu 600 | 581 G1yL - - - 1741 GGTA | оу Об |
| 2761 GATA | מ ט ג | LeuTyrGlnGluSerThrSerLysSerAlaLeuSerGlnGluPheGluAlaPhePheGln 580 | 561 LeuT 1681 TTAT | Db dg |
| | Db s | hrGluGlnGluIleLeuLysAlaIleAsnIleAsnSerPheValGluCysGlyIleHis 560 | 541 ThrG 1621 ACTG | Db Oy |
| 2641 CTCA | מם אל | euSerIleAlaLysArgProLeuTrpArgGlnGluSerLeuGlnSerValLysAsnThr 540 | 521 LeuSerIle 1561 CTTTCCATC | Qy Db |
| | d d | AlaThrargAlaValMetLysHisLeuAlaAlaValTyrGlnHisGlyCysLeuLeuGly 520 | 501 AlaT 1501 GCCA | Оy |
| | 0 D K | @rAspIleThrSerThrTyrSerSerLeuLeuArgTyrThrCysGlySerSerValGlu 500 | 481 SerA 1441 TCGG | Оy |
| 2461 GACC | O D X | erHisGluProGluGluValThrLysGlyAsnGlyTyrLeuGlnLysMetValSerIle 480 | 461 SerHis | P 0y |
| 2401 TTGT | מם א | PhePheHisLysSerPheGlnGluTyrThrAlaGlyArgArgLeuSerSerLeuLeuThr 460 | 441 PheP 1321 TTCT | Db Qy |
| | Db C | LeuLeuThrThrGlyLeuLeuCysLysTyrThrAlaGlnArgPheLysProLysTyrLys 440 | 421 LeuL 1261 CTGC | Оу |
| 1 28 1 | 0 da | ValPheSerHisLysPheAspPheGluLeuGlnAspValSerSerValAsnGluAspVal 420 | 401 ValP 1201 GTGT | Qу Дъ |
| 2 H | מם מע | /alalaalaSerAspPheIleArgSerLeuAspHisCysGlyAspLeuAlaLeuGluGly 400 | 381 Vala 1141 GTGG | Db Oy |
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CURRENT
  FILING
T: Bertin, John
T: Robison, Keith E.
INVENTION: NOVEL MOLECULES OF THE
INVENTION: PROTEIN FAMILY AND USE
RENNCE: 07334-136001
APPLICATION NUMBER: US/09/697,089
FILING DATE: 2000-10-26
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 3072
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ORGANISM: 1
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TYPE: DN
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  IleGluAlaLeuIleLysGluAsnHisArgPheLysAsnMetValIleValThrThr
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| 640 | MetAlaSerTrpGluLysAlaAlaGluAspThrGlyGlyIleHisMetGluGluAlaPro | 621 | Qy |
|------|---|------|-------|
| 1860 | CATTTGCCCAATTGTGCAAGTGCTCTGGACTTCATTAAACTGGACTTTTATGGGGGAGCT | 1801 | рb |
| 620 | isLeuProAsnCysAlaSerAlaLeuAspPheIleLysLeuAspPheTyrGlyGlyAl | 601 | Qy |
| · 00 | ACTICIT | | Db es |
| 5 | lvivsserienTvrileAsesserGlvAseTleDroAseTvrienDheAseDheDheG | | 0 1 |
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| 00 | euTyrGlnGluSerThrSerLysSerAlaLeuSerGlnGluPheGluAlaPhePheGl | on i | Qy ! |
| 1680 | | N | Дb |
| 560 | $\verb hrGluGlnGluIleLeuLysAlaIleAsnIleAsnSerPheValGluCysGlyIleHi$ | 541 | Qy |
| 1620 | CTTTCCATCGCCAAGAGGCCTCTCTGGAGACAGGAATCTTTGCAAAGTGTGAAAAAACACC | 1561 | Db |
| 540 | euSerIleAlaLysArgProLeuTrpArgGlnGluSerLeuGlnSerValLysAsnTh | 521 | Qy |
| 1560 | GCCACCAGGGCTGTTATGAAGCACCTCGCAGCAGTGTATCAACACGGCTGCCTTCTCGGA | 1501 | Db |
| 520 | laThrArgAlaValMetLysHisLeuAlaAlaValTyrGlnHisGlyCysLeuLeuGl | 501 | Qy |
| 1500 | TCGGACATTACATCCACTTATAGCAGCCTGCTCCGGTACACCTGTGGGTCATCTGTGGAA | 1441 | Db |
| 500 | erasplleThrSerThrTyrSerSerLeuLeuArgTyrThrCysGlySerSerValGl | 481 | Qy |
| 1440 | TCTCATGAGCCAGAGGAGGTGACCAAGGGGAATGGTTACTTGCAGAAAATGGTTTCCATT | 1381 | Db |
| 480 | erHisGluProGluGluValThrLysGlyAsnGlyTyrLeuGlnLysMetValSerIl | 461 | Qy |
| 1380 | TTCTTTCACAAGTCATTCCAGGAGTACACAGCAGGACGAAGACTCAGCAGTTTATTGACG | 1321 | Db |
| 460 | hePheHisLysSerPheGlnGluTyrThrAlaGlyArgArgLeuSerSerLeuLeuTh | 441 | Qy |
| 1320 | TGACAACTGGGCTCCTCTGAAATATACAGCTCAAAGGTTCAAGCCAAAGTA | 1261 | Дb |
| 440 | euLeuThrThrGlyLeuLeuCysLysTyrThrAlaGlnArgPheLysProLysTyrLy | 421 | Оу |
| 1260 | GTGTTCTCCCACAAGTTTGATTTCGAACTGCAGGATGTGTCCAGCGTGAATGAGGATGTC | 1201 | Db |
| 420 | alPheSerHisLysPheAspPheGluLeuGlnAspValSerSerValAsnGluAspVa | 401 | Qy |
| 1200 | GTGGCTGCAAGTGACTTCATTCGGAGCCTGGACCCACTGTGGAGACCTAGCTCTGGAGGGT | 1141 | Db |
| 400 | alAlaAlaSerAspPheIleArgSerLeuAspHisCysGlyAspLeuAlaLeuGluGl | 381 | Qy |
| 1140 | ACGCTGTTCCATACCTTCTATGATCTGTTGATACAGAAAAAAAA | 1081 | Db |
| 380 | rLeuPheHisTh r PheT yr AspLeuLeuIleGlnL y sAsnL y sHisL y sHisL y sGl | 361 | Qy |
| 1080 | TCATCACTTGTGCAATCCAGATGGGTGAAAGTGAGTTCCACTCTCACACACA | 1021 | Db |
| 360 | ${\tt alValIleThrCysAlaIleGlnMetGlyGluSerGluPheHisSerHisThrGlnTerm}$ | 341 | Qy |
| 1020 | TTGTTGCTCCAAATTCAGAAATCCAGGTGCTTGAGGAATCTCATGAAGACCCCTCTCTTT | 961 | Db |
| 340 | uLeuLeuGlnIleGlnLysSerArgCysLeuArgAsnLeuMetLysThrProLeuPh | 321 | Qy |
| 960 | ACAGAAGACAGCGCCCAGGCTCTCATCCGAGAAGTGCTGATCAAGGAGCTTGCTGAAGGC | 901 | Дb |
| 320 | hrGluAspSerAlaGlnAlaLeuIleArgGluValLeuIleLysGluLeuAlaGlu | 301 | Qy |
| 900 | ACTGAGTGCCTGAGGCACATACGGCAGTTTGGTGCCCTGACTGCTGAGGTGGGGGGATATG | 841 | В |
| 300 | rGluCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMe | 281 | VQ |
| 840 | | 781 | Db |

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Best Local Similarity:
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TITLE OF INVENTION: NOVEL MOLECULES OF THE C
FILE REFERENCE: 0734-329001
CURRENT APPLICATION NUMBER: US/09/841,739
CURRENT FILING DATE: 2001-08-29
PRIOR APPLICATION NUMBER: US 09/697,089
PRIOR FILING DATE: 2000-10-26
PRIOR APPLICATION NUMBER: US 60/161,822
PRIOR FILING DATE: 1999-10-27
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PastSEQ for Windows Version 4.0
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| CGGACATTACATCCACTTATAGCAGCCTGCTCCGGTACACCTGTGGGTCATCTGTGG LaThrArgAlaValMetLysHisCeuAlaAlaValTyrGlnHisGlyCysLeuLeuG | SerHisGluProGluGluValThrLysGlyAsnolyTyrLeuGlnLysMetValSerIle 48 | 421 LeuLeuThrThrGlyLeuLeuCysLysTyrThrAlaGlnArgPheLysProLysTyrLys 440 | 381 ValalaalaSerAspPheIleArgSerLeuAspHisCysGlyAspLeuAlaLeuGluGly 400 | 341 ValVallleThrCysAlaIleGlnMetGlyGluSerGluPheHisSerHisThrGlnThr 360 | 301 ThrGluAspSerAlaGlnAlaLeuIleArgGluValLeuIleLysGluLeuAlaGluGly 320 | 261 IleGluAlaLeuIleLysGluAsnHisArgPheLysAsnMetValIleValThrThrThr 280 | | ASPILEPTOCLYTHILLER III AND THE PROCESS OF THE PROC |
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| 61 GluLysAspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGluGln 8 | 821 AspLeuGluIleGlnLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeu 840 | /81 LIELYSLEINAIGGLYLEILYSASILEULYSLYSMECTYSLEUPREHISLEUTINTHIS 800 | 41 LeuSerIIeHisAspLeuGlnAsnGlnArgLeuProclyGlyLeuThrAspSerLeuGly [| 01 GCTGGAAGCCTCACCATAGAAGATGAGAGGCACATCACATCTGTAACAAACCTGAAACACCCATCCCTCAAACAACATTTATTCTCTCATGGTGGAA 2 21 AlaSerProLeuThrIleGluAspGluArgHisIleThrSerValThrAsnLeuLysThr 7 | 81 ACTCTC 81 GlyLys 41 GGGAAA | | 1741 GGTAAAAGCTTATATATATCAACTCAGGGAACATCCCCGATTACTTATTTGACTTCTTTGAA 1800 601 HisLeuProAsnCysAlaSerAlaLeuAspPheIleLysLeuAspPheTyrGlyGlyAla 620 | 61 CTTTCCATCGCCAAGAGGCCCTCTCTGGAGACAGGAATCTTTGCAAAGTGTGAAAAACACC 16 41 ThrGluGlnGluIleLeuLysAlaIleAsnIleAsnSerPheValGluCysGlyIleHis 56 |

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GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
FILE REFERENCE: 07334-136W01
CURRENT APPLICATION NUMBER: PCT/US00/29643
CURRENT APPLICATION NUMBER: PCT/US00/29643
CURRENT FILING DATE: 1990-10-26
PRIOR APPLICATION NUMBER: US 60/161,822
PRIOR FILING DATE: 1999-10-27
                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 11

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 1

LENGTH: 3133

TYPE: DNA

ORGANISM: Homo sapiens
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| SerLeuAspHisCysGlyAspLeuAlaLeuGluGly 400 | ValAlaAlaSerAspPheIle | · | δõ |
| DeuLeuileGlnLysAsnLysHisLysHisLysGly 380 | ThrLeuPheHisThrPheTyr | y 361 b 1116 | 4d 60 |
| EGLYGLUS GGGTGAAA | TTGI | 10 | Db Q |
| GTGCTTGAGGAATCTCATGAAGACCCCTCTCTTT 10 | GTTGCTCCAAATTCAGAA | 99 | 멍 |
| gAsnLeuMetLysThrP | LeuLeuLeuGlnIleGlnLys | у 321 | 0 |
| ULLEATGGINVAILEUILELYSGIULEUALAGIUGIY 320 | ThrGluAspSerAlaGLnAla | y 301 b 936 | ρ ₀ ολ |
| AGTTTGGTGCCCTGACTGCTGAGGTGGGGGATATG 93 | GAGTGCCTGAGGCACAT | 87 | D |
| gGlnPheGlyAlaLeuThrAlaGluValGlyAspMet 300 | ThrGluCysLeuArgHisIle | N | Ø |
| CACCGCTTCAAGAACATGGTCATCGTCACCACCTACC 875 | ATCGAAGCCCTGATAAAGGAAAA | _ | Db |
| isArgPheLysAsnMetValIleValThrThrTh | leGluAlaLeuIleLysGl | 2 | ø |
| <u> </u> | CAGAGGGTTCTTTTCCTTCTT | 7 | 문 : |
| yTyrAsnGluPheLysProGlnAsnCysProGlu 2 | rgValLeuPheLeuI | N | Ö |
| 5 | CTGGATATACCTGGCACAATC | 69 | Db ? |
| sGlnThrPheMetAlaMetLeuLeuLysLeuArg 24 | LeuAspIleProGlyThrIl | 22 | o o |
| CAGGGTGGACTTTTTGAAACCCTCTGTGATCAACTC | FIREFIRE LEUAL GLEUSEL AL 9A | b 636 | ט ג |
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| GlyLysCysLysAlaLeuThrLysPheLysPheVal 200 | ArgileAlaMetLeuTrpGly | y 181 b 576 | dg Vo |
| ATCTGGCAAAGGCAAGTCCACTCTGCTGCA | CTTCAGAGCCCCTGCATCAT | | D |
| GlyGluSerGlyLysGlyLysSerThrLeuLeuGln 180 | - H | -ب | Qy |
| GTGGAGCAGCTGACCCTGAATGGCCTCCTGCAGGCT 515 | AGGAAGGACCAACACCATCAC | - | Дb |
| alGluGlnLeuThrLeuAsnGlyLeuLeuGlnAl | ArgLysAspGlnHisH | <u></u> | VΩ |
| AACTTGAAAAGCACCTTCACAGAACCTGTCCTGTGG 455 | GGTGAAGATATTGACATTATTT | ω | ДD |
| snLeuLysSerThrPheThrGluProValLeuTr | GlyGluAspIleAspIleI | у 121 | Qy |
| GTACCATACCCCATCTTTCTGAACTTTTATCCCCTT 395 | TTGGCTCAGGATTTAAAGGAC | | Db |
| rHisThrProSerPheLeuAsnPheTyrProLe | LeuAlaGlnAspLeuLysAs | <u> </u> | VΩ |
| | | N | Db |
| eHisGlnThrSerGluGlyAspLeuAspAs | PheGlnAspLeuAsnGlyG | у 81 | δō |
| TITTCTTAAATCCCTTAAGGAGTGGAACTATCCTCTA 275 | AAGGGTTCAGAGTCCTGTAAC | b 216 | ם |
| uLysSerLeuLysGluTrpAsnTyrProLe | ysGlySerGluSerCys | у 61 | δō |
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TITLE OF INVENTION: NOVEL MOLECULES
TITLE OF INVENTION: PROTEIN FAMILY
FILE REFERENCE: 07334-136001
                                                       SOFTWARE: FastSEQ
SEQ ID NO 1
LENGTH: 3133
                                                                                                                           CURRENT APPLICATION NUMBER: US/09/697,089
CURRENT FILING DATE: 2000-10-26
                                                                                                                                                                                      APPLICANT: Bertin, John APPLICANT: Robison, Ke
ORGANISM: HOMO: FEATURE: NAME/KEY: CDS LOCATION: (36).
                                                                                                     PRIOR APPLICATION NUMBER: US PRIOR FILING DATE: 1999-10-27
                                                                                            NUMBER OF SEQ ID NOS:
                                              TYPE: DNA
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| lignment Scores: red. No.: 0 | US-09-697-089-2 (1-1024) x US-09-697-089-1 (1-3133) | Oy 1 MetAsnPheIleLysAspAsnSerArgAlaLeuIleGlnArgMetGlyMetThrValIle 20 | Qy 21 LysGlnIleThrAspAspLeuPheValTrpAsnValLeuAsnArgGluGluValAsnIle 40 | Qy 101 LeualaGlnAspLeuLysAspLeuTyrHisThrProSerPheLeuAsnPheTyrProLeu 120 | Qy 121 GlyGluAspIleAspIleIlePheAsnLeuLysSerThrPheThrGluProValLeuTrp 140 | Qy 141 ArgLysAspGlnHisHisHisArgValGluGlnLeuThrLeuAsnGlyLeuLeuGlnAla 160 | Qy 161 LeuGlnSerProCysIleIleGluGlyGluSerGlyLysGlyLysSerThrLeuLeuGln 180 | Qy 181 ArgileAlaMetLeuTrpGlySerGlyLysCysLysAlaLeuThrLysPheLysPheVal 200 | Qy 201 PhePheLeuArgLeuSerArgAlaGlnGlyGlyLeuPheGluThrLeuCysAspGlnLeu 220 | Qy 221 LeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLysLeuArg 240 | Qy 241 GlnArgValLeuPheLeuLeuAspGlyTyrAsnGluPheLysProGlnAsnCysProGlu 260 | Qy 261 IleGluAlaLeuIleLysGluAsnHisArgPheLysAsnMetValIleValThrThrThr 280 | Qy 281 ThrGluCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMet 300 | Qy 301 ThrGluAspSerAlaGlnAlaLeuIleArgGluValLeuIleLysGluLeuAlaGluGly 320 | ignment ed. No. Sore: So | Similarity: 100.00% Conservative: 0 Similarity: 100.00% Conservati | 20 40 95 115 115 215 215 275 275 395 1120 395 1120 395 1120 395 1120 395 1120 395 1120 395 1120 395 1140 1155 1155 1155 1155 1155 1155 115 |
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| Gaps: 0 -09-697-089-2 (1-1024) x US-09-697-089-1 (1-3133) 1 MetAsnPheIleLysAspAsnSerArgAlaLeuIleGlnArgMetGlyMetThrValIle 20 | 1 MetasnPheIleLysAspAsnSerArgAlaLeuIleGlnArgMetGlyMetThrValIle 20 | 21 LysGlnIleThrAspAspLeuPheValTrpAsnValLeuAsnArgGluGluValAsnIle 40 | | 61 LysGlySerGluSerCysAsnLeuPheLeuLysSerLeuLysGluTrpAsnTyrProLeu 80 | 61 LysGlySerGluSerCysAsnLeuPheLeuLysSerLeuLysGluTrpAsnTyrProLeu | 61 LysGlySerGluSerCysAsnLeuPheLeuLysSerLeuLysGluTrpAsnTyrProLeu | 61 LysGlySerGluSerCysAsnLeuPheLeuLysSerIeuLysGluTrpAsnTyrProLeu | 61 LysGlySerGluSerCysAsnLeuPheLeuLysSerLeuLysGluTrpAsnTyrProLeu | 61 LysGlySerGluSerCysAsnLeuPheLeuLysSerLeuLysGluTrpAsnTyrProLeu | 15 | leCysCysGluLysValGluGlnAspAlaAlaArgGlyIleIleHisMetIleLeuLy | 1 |
| Gaps: 0 -09-697-089-2 (1-1024) x US-09-697-089-1 (1-3133) 1 MetAsnPheileLysAspAsnSerArgAlaLeuIleGlnArgMetGlyMetThrValIle 20 | 1 MetAsnPheIleLysAspAsnSerArgAlaLeuIleGlnArgMetGlyMetThrValIle 20 | 21 LysGlnIleThrAspAspLeuPheValTrpAsnValLeuAsnArgGluGluValAsnIle 40 | 41 IleCysCysGluLysValGluGlnAspAlaAlaArgGlyIleIleHisMetIleLeuLys 60 | 81 PheGlnAspLeuAsnGlyGlnSerLeuPheHisGlnThrSerGluGlyAspLeuAspAsp | 81 PheGlnAspLeuAsnGlyGlnSerLeuPheHisGlnThrSerGluGlyAspLeuAspAsp | 81 PheGlnAspLeuAsnGlyGlnSerLeuPheHisGlnThrSerGluGlyAspLeuAspAsp | 81 PheGlnAspLeuAsnGlyGlnSerLeuPheHisGlnThrSerGluGlyAspLeuAspAsp | 81 PheGinAspLeuAsnGlyGinSerLeuPheHisGinThrSerGluGlyAspLeuAspAsp | ### PheGlnAspLeuAsnGlyGlnSerLeuPheHisGlnThrSerGluGlyAspLeuAspAsp | 21 | ysGlySerGluSerCysAsnLeuPheLeuLysSerLeuLysGluTrpAsnTyrProLe | 7 |
| Gaps: 0 -09-697-089-2 (1-1024) x US-09-697-089-1 (1-3133) 1 MetasnPheIleLysAspAsnSerArgAlaLeuIleGlnArgMetGlyMetThrValIle 20 | 1 MetasnPheileLysAspAsnSerargAlaLeuIleGlnArgMetGlyMetThrValIle 20 | 21 LysGlnIleThrAspAspLeuPheValTrpAsnValLeuAsnArgGluGluValAsnIle 40 | 41 IleCysCysGluLysValGluGlnAspAlaAlaArgGlyIleIleHisMetIleLeuLys 60 | | 101 LeuAlaGlnAspLeuLysAspLeuTyrHisThrProSerPheLeuAsnPheTyrProLeu 12 | 101 LeualaGlnaspLeuLysaspLeuTyrHisThrProSerPheLeuasnPheTyrProLeu 12 | 101 LeuAlaGlnAspLeuLysAspLeuTyrHisThrProSerPheLeuAsnPheTyrProLeu 12 | 101 LeuAlaGlnAspLeuLysAspLeuTyrHisThrProSerPheLeuAsnPheTyrProLeu | 101 LeuAlaGlnAspLeuLysAspLeuTyrHisThrProSerPheLeuAsnPheTyrProLeu | 101 LeuAlaGlnAspLeuLysAspLeuTyrHisThrProSerPheLeuAsnPheTyrProLeu | 101 LeuAlaGlnAspLeuLysAspLeuTyrH1SThrProSerPheLeuAsnPheTyrProLeu | 101 LeuAlaGlnAspLeuLysAspLeuTyrHlsThrProSerPheLeuAsnPheTyrProLeu | 101 LeuAlaGlnAspLeuLysAspLeuTyrH1SThrProSerPheLeuAsnPheTyrProLeu | 101 LeuAlaGlnAspLeuLysAspLeuTyrHisThrProSerPheLeuAsnPheTyrProLeu 12 | 81 276 | nAspLeuAsnGlyGlnSerLeuPheHisGlnThrSerGluGlyAspLeuAspAs | 100 335 |

| 680 | ThrLeuGluValThrLeuArgAspPheSerLysLeuAsnLysGlnAspIleThrTyrLeu | 661 | Qy |
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| 660 | GluThrTyrIleProSerArgAlaValSerLeuPhePheAsnTrpLysGlnGluPheArg | 641 | Qy |
| 201 | | 1956 | Db |
| 640 | MetalaSerTrpGluLysalaAlaGluAspThrGlyGlyIleHisMetGluGluAlaPro | 621 | Qy |
| 1955 | | 1896 | Db |
| 620 | HisleuProAsnCysAlaSerAlaLeuAspPheIleLysLeuAspPheTyrGlyGlyAla | 601 | Qy |
| 1895 | | 1836 | Db |
| 1835 | GlyLysSerLeuTyrIleAsnSerGlyAsnIleProAspTyrLeuPheAspPhePheGlu | 581 | da |
| | | 1776 | Vy |
| 580 | LeuTyrGlnGluSerThrSerLysSerAlaLeuSerGlnGluPheGluAlaPhePheGln | 561 | Qy |
| 1775 | | 1716 | Db |
| 560 | ThrGluGlnGluIleLeuLysAlaIleAsnIleAsnSerPheValGluCysGlyIleHis | 541 | Qy |
| 1715 | | 1656 | Db |
| 540 | LeuSerIleAlaLysArgProLeuTrpArgGlnGluSerLeuGlnSerValLysAsnThr | 521 | Qy |
| 1655 | | 1596 | Db |
| 520 | AlaThrArgAlaValMetLysHisLeuAlaAlaValTyrGlnHisGlyCysLeuLeuGly | 501 | Qy |
| 1595 | | 1536 | Db |
| 500 | SerAspIleThrSerThrTyrSerSerLeuLeuArgTyrThrCysGlySerSerValGlu | 481 | Qy |
| 1535 | | 1476 | Db |
| 480 | SerHisGluProGluGluValThrLysGlyAsnGlyTyrLeuGlnLysMetValSerIle | 461 | Qy |
| 1475 | | 1416 | Db |
| 460 | PhePheHisLysSerPheGlnGluTyrThrAlaGlyArgArgLeuSerSerLeuLeuThr | 441 | Qy |
| 1415 | | 1356 | Db |
| 440 | LeuLeuThrThrGlyLeuLeuCysLysTyrThrAlaGlnArgPheLysProLysTyrLys | 421 | Qy |
| 1355 | | 1296 | Db |
| 420 | ValPheSerHisLysPheAspPheGluLeuGlnAspValSerSerValAsnGluAspVal | 401 | Qy |
| 1295 | | 1236 | Db |
| 400 | ValalaalaSerAspPheIleArgSerLeuAspHisCysGlyAspLeuAlaLeuGluGly | 381 | Qy |
| 1235 | | 1176 | Db |
| 380 | ThrLeuPheHisThrPheTyrAspLeuLeuIleGlnLysAsnLysHisLysHisLysGly | 361 | Qy |
| 1175 | | 1116 | Db |
| 360 | ValValIleThrCysAlaIleGlnMetGlyGluSerGluPheHisSerHisThrGlnThr | 341 | Qy |
| 1115 | | 1056 | Db |
| 340 | LeuLeuLeuGlnIleGlnLysSerArgCysLeuArgAsnLeuMetLysThrProLeuPhe | 321 | Qy |
| 1055 | | 996 | Db |
| 995 | | 936 | Db |

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CURRENT FILING DATE: 2001-08-29
PRIOR APPLICATION NUMBER: US 09/697,089
PRIOR FILING DATE: 2000-10-26
PRIOR APPLICATION NUMBER: US 60/161,822
PRIOR FILING DATE: 1999-10-27
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
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GENERAL INFORMATION:
APPLICANT: Bertin, John
TITLE OF INVENTION: NOVEL MODEL FILE REFERENCE: 07334-329001
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TYPE: DNA
ORGANISM: Homo
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NAME/KEY: CDS
LOCATION: (36)
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                                                                   LeuAlaGlnAspLeuLysAspLeuTyrHisThrProSerPheLeuAsnPheTyrProLeu
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| 500 1535 | 481 SerāspīleThrSerThrTyrSerSerLeuLeuArgTyrThrCysGlySerSerValGlu | Оу |
| 480 1475 | 461 SerHisGluProGluGluValThrLysGlyAsnGlyTyrLeuGlnLysMetValSerIle | Qу |
| 460 1415 | 441 PhePheHisLysSerPheGlnGluTyrThrAlaGlyArgArgLeuSerSerLeuLeuThr | Фу |
| 440 1355 | 421 LeuLeuThrThrGlyLeuLeuCysLysTyrThrAlaGlnArgPheLysProLysTyrLys | Qy |
| 420 1295 | 401 ValPheSerHisLysPheAspPheGluLeuGlnAspValSerSerValAsnGluAspVal | Оу |
| 400 1235 | 381 ValAlaAlaSerAspPheIleArgSerLeuAspHisCysGlyAspLeuAlaLeuGluGly | Ωу |
| 380 1175 | 361 ThrLeupheHisThrPheTyrAspLeuLeuIleGlnLysAsnLysHisLysHisLysGly | Оγ |
| 360 1115 | 341 ValVallleThrCysAlaIleGlnMetGlyGluSerGluPheHisSerHisThrGlnThr | Ф |
| 340 1055 | 321 LeuLeuGlnIleGlnLysSerArgCysLeuArgAsnLeuMetLysThrProLeuPhe | Дb |
| 320 995 | 01 ThrGluAspSerAlaGlnAlaLeuIleArgGluValLeuIleLysGluLeuAlaGluGly | Оy |
| 300 935 | 281 ThrGluCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMet | Qу Дъ |
| 280 875 | 261 IleGluAlaLeuIleLysGluAsnHisArgPheLysAsnMetValIleValThrThrThr | Qу Дъ |
| 260 815 | 241 GlnArgValLeuPheLeuLeuAspGlyTyrAsnGluPheLysProGlnAsnCysProGlu | Оу |
| 240 755 | 221 LeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLysLeuArg | DЬ |
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RESULT 7

US-10-156-733-1

US-10-156-733-1

Sequence 1, Application US/1015673:
SEMERAL INFORMATION:

APPLICANT: Alnemri, Emad S.

TITLE OF INVENTION: IPAF, AN ICE-
TITLE OF INVENTION: FACTOR
FILE REFERENCE: 480140.477

CURRENT FALLING DATE: 2002-05-24

NUMBER OF SEQ ID NOS: 14

POPTMARE: FASTSEQ for Windows Ve
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Pred. No.:
Score:
Score:
Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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                                                          ValAlaAlaSerAspPheIleArgSerLeuAspHisCysGlyAspLeuAlaLeuGluGly
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 CAGAGGGTTCTTTTCCTTGATGGCTACAATGAATTCAAGCCCCAGAACTGCCCAGAA
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                                                                                                            MetAlaSerTrpGluLysAlaAlaGluAspThrGlyGlyIleHisMetGluGluAlaPro
                                                                                                                                                           CATTTGCCCAATTGTGCAAGTGCCCTGGACTTCATTAAACTGGACTTTTATGGGGGGAGCT
                                                                                                                                                              HisteuProAsnCysAlaSerAlaLeuAspPheIleLysLeuAspPheTyrGlyGlyAla
                                                              GCCAGTCCCCTCACCATAGAAGATGAGAGGCACATCACATCTGTAACAAACCTGAAAACC
                                                                                                                                           ATGGCTTCATGGGAAAAGGCTGCAGAAGACACAGGTGGAATCCACATGGAAGAGGCCCCA
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; LENGTH: 3219
; TYPE: DNA
; ORGANISM: HOMO:
US-10-156-733-14
                                                                                                                                                     Sequence 14, Application US/10156733
(GENERAL INFORMATION:
APPLICANT: Alinemri, Emad S.
TITLE OF INVENTION: IPAF, AN ICE-PROTEAS
TITLE OF INVENTION: FACTOR
FILE REFERENCE: 480140.477
CURRENT APPLICATION NUMBER: US/10/156,73
CURRENT FILING DATE: 2002-05-24
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 4.
SEQ ID NO 14
LENGTH: 3219
                                                                                            Alignment
Pred. No.:
                                        Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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                    US-09-697-089-2
                                                                                 Score:
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Matches:
Conservative:
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DP QA В Qy В δ Дb

| PheHisSerHisThrG | TeuLeuLeuGlnIleGlnLysSerArgCysLeuArgAsnLeuMetLysThrProLeuP | GAGTGCCTGAGGCACATACGGCAGTTTGGTGCCCTGACTGCTGAGGTGGGGGATATG | 81 ThrGluCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMet 3 | 61 IleGluAlaLeuIleLySGluAsnHisArgPheLysAsnMetValIleValThrThrThr 2 | 41 GlnargValLeuPheLeuLeuAspGlyTyrAsnGluPheLysProGlnAsnCysProGlu 2 | LeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLysLeuArg 2 | yGlyLeuPheGluThrL GGACTTTTTGAAACCC | rgIleAlaMetLeuTrpGlySerGlyLysCysLysAlaLeuThrLysPheLysPheVal 2 | 161 LeuGlnSerProCysIleIleGluGlyGluSerGlyLysGlyLysSerThrLeuLeuGln 180 | 141 ArgLysAspGlnHisHisHisArgValGluGlnLeuThrLeuAsnGlyLeuLeuGlnAla 160 | 21 GlyGluAspIleAspIleIlePheAsnLeuLysSerThrPheThrGluProValLeuTrp 1 | 01 LeuAlaGlnAspLeuLysAspLeuTyrHisThrProSerPheLeuAsnPheTyrProLeu 1 | 81 PheGInAspLeuAsnGlyGlnSerLeuPheHisGlnThrSerGluGlyAspLeuAspAsp 1 | 1 LysGlySerGluSerCysAsnLeuPheLeuLysGerLeuLysGluTrpAsnTyrProLeu 8 | 31uG1nAspAlaAlaArgG1yIleIle | 21 LysGlnIleThrAspAspLeuPheValTrpAsnValLeuAsnArgGluGluValAsnIle 40 | |
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| 701 AlaGlySerLeuSerLeuValLeuSerThrCysLysAsnleflyrSerLeuMetValGlu 720 | 1 GlyLysIlePheSerSerAlaThrSerLeuArgLeuGlnIleLysArgCysAlaGlyVal 70 | 661 ThrLeuGluValThrLeuArgAspPheSerLysLeuAsnLysGlnAspIleThrTyrLeu 680 | 641 GluThrTyrIleProSerArgAlaValSerLeuPhePheAsnTrpLysGlnGluPheArg 660 | 621 MetAlaSerTrpGluLysAlaAlaGluAspThrGlyGlyIleHisMetGluGluAlaPro 640 | 601 HisLeuProAsnCysAlaSerAlaLeuAspPheIleLysLeuAspPheTyrGlyGlyAla 620 | 581 GlyLysserLeuTyrIleAsnSerGlyAsnIleProAspTyrLeuPheAspPhePheGlu 600 | 561 LeuTyrGlnGluSerThrSerLysSerAlaLeuSerGlnGluPheGluAlaPhePheGln 580 | 41 ThrGluGlnGluIleLeuLysAlaIleAsnIleAsnSerPheValGluCysGlyIleHis 5 | 521 LeuSerIleAlaLysArgProLeuTrpArgGlnGluSerLeuGlnSerValLysAsnThr 540 | 501 AlaThrargAlaValMetLysHisLeuAlaAlaValTyrGlnHisGlyCysLeuLeuGly 520 | 81 SerAspIleThrSerThrTyrSerSerLeuLeuArgTyrThrCysGlySerSerValGlu 5 | 461 SerHisGluProGluGluValThrLysGlyAsnGlyTyrLeuGlnLysMetValSerIle 480 | 441 PhePheHistysSerPheGlnGluTyrThrAlaGlyArgArgLeuSerSerLeuLeuThr 460 | 421 LeuLeuThrThrGlyLeuLeuCysLysTyrThrAlaGlnArgPheLysProLysTyrLys 440 | 401 ValPheSerHisLysPheAspPheGluLeuGlnAspValSerSerValAsnGluAspVal 420 | GCT GCT | 25 ACGCTGTTCCATACCTTCTATGATCTGTTGATACAGAAAAACAAAC |

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Sequence 23, Application PC/TUS0107143
GENERAL INFORMATION:
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LENGTH: 3213
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PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/188,916
PRIOR FILING DATE: 2000-03-13
PRIOR APPLICATION NUMBER: 60/237,846
PRIOR APPLICATION DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
RIGHER OF SEQ ID NOS: 52
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                                       LeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLysLeuArg
                                                                        GlyGluAspIleAspIleIlePheAsnLeuLySSerThrPheThrGluProValLeuTrp 140
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                        CTGGATATACCTGGCACAATCAGGAAGCAGACATTCATGGCCATGCTGCTGAAGCTGCGG
                                                                                                                              CGAATTGCCATGCTCTGGGGGCTCCGGAAAGTGCAAGGCTCTGACCAAGTTCAAATTCGTC
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| TCA | GlyLysSerLeuTyrIleAsnSerGlyAsnIleProAspTyrLeuPheAspPheP | 187 | dd Qy |
|-----------------------------------|--|-------------|----------|
| TCAA 187 | | п | |
| heGln 580 | 1 LeuTyrGlnGluSerThrSerLysSerAlaLeuSerGlnGluPheGluAlaPhePh | 56 181 | d Vo |
| leHis 560 CCAT 1818 | 1 ThrGluGluGluIleLeuLysAlaIleAsnIleAsnSerPheValGluCysGlyIl | 54 175 | Qу |
| snThr 540 ACACC 1758 | 1 LeuSerIleAlaLysArgProLeuTrpArgGlnGluSerLeuGlnSerValLysAs | 9 2 | dg Vo |
| euGly 520 CGGA 1698 | 1 AlaThrArgAlaValMetLysHisLeuAlaAlaValTyrGlnHisGlyCysLeuLe | 163 | DP 6A |
| alGlu 500 GGAA 1638 | 1 SerAspileThrSerThrTyrSerSerLeuLeuArgTyrThrCysGlySerSerVa | 48 157 | Qy dg |
| Prile 480 CATT 1578 | 1 SerHisGluProGluGluValThrLysGlyAsnGlyTyrLeuGlnLysMetValSe | 46 151 | Dβ |
| euThr 460 GACG 1518 | PhePheHisLysSerPheGlnGluTyrThrAlaGlyArgArgLeuSerSerLeuLe | 441 1459 | Qy db |
| /rLys 440 ATAAA 1458 | LeuLeuThrThrGlyLeuLeuCysLysTyrThrAlaGlnArgPheLysProLysTy | 421 1399 | 99 VQ |
| spVal 420 \TGTC 1398 | ValPheSerHisLysPheAspPheGluLeuGlnAspValSerSerValAsnGluAs | 401 1339 | Db Qy |
| uGly 400 GGGT 1338 | ValAlaAlaSerAspPheIleArgSerLeuAspHisCysGlyAspLeuAlaLeuGl | 381 1279 | Оy |
| 'SGLY 380 AGGT 1278 | ThrLeuPheHisThrPheTyrAspLeuLeuIleGlnLysAsnLysHisLysHisLy | 361 1219 | Ф |
| .nThr 360 AACA 1218 | ValVallleThrCysAlaIleGlnMetGlyGluSerGluPheHiSSerHisThrGl | 341 1159 | Qy Db |
| uPhe 340 CTTT 1158 | LeuLeuLeuGlnIleGlnLysSerArgCysLeuArgAsnLeuMetLysThrProLe | 321 1099 | Db Qy |
| uGly 320 AGGC 1098 | ThrGluAspSerAlaGlnAlaLeuIleArgGluValLeuIleLysGluLeuAlaGluHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH | 30. 1039 | ОУ |
| PMet 300 TATG 1038 | ThrGluCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAsj | 281 979 | Оу |
| TACC 978 | IleGluAlaLeuTleLysGluAsnHisArgPheLysAsnMetVallleValThrTh: | 261 919 | ФФ |
| 1111 AGAA 918 | | 859 | Db |

| 980 307 | . PheGluAsnLeuLysGlnLeuValPhePheAspPheSerThrLysGluF | 96 | Оу |
|------------|--|-------------|----------|
| w w | 1 GlnLeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTrpLeuAlaPheMetGlyVal | 941 2959 | Qy |
| 94 | AspThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPheGln | 921 | ФР |
| 29 | | 2899 | |
| 92 | LysHisLeuGluGluValProGlnLeuValLysLeuGlyLeuLysAsnTrpArgLeuThr | 901 | Qy |
| 28 | | 2839 | |
| 90 | LeuThrAlaLeuMetLeuProTrpGlyCysAspValGlnGlySerLeuSerSerLeuLeu | 881 | Qу |
| 28 | | 2779 | Дъ |
| 88 | . GluLysAspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGluGln | 861 | Qу |
| 27 | | 2719 | |
| 86 | . AlaGlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeu | 841 | Qу |
| 27 | | 2659 | |
| 26 | . AspLeuGluGluIleGlnLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeu | 821 | Qy |
| | | 2599 | Db |
| 25 | LeuSerAsp11eGlyGluGlyMetAspTyrI1eValLysSerLeuSerSerGluProCys | 801 2539 | Qy Db |
| 80 25 | IleLysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHis | 781 2479 | Оу |
| 78 | ASDLEULYSASDLEUThrLYSLEUIleMetASpASDIleLYSMetASDGluGluAspAla | 761 | Qy |
| 24 | | 2419 | Db |
| 76 24 | LeuSerIleHisAspLeuGlnAsnGlnArgLeuProGlyGlyLeuThrAspSerLeuGly | 741 2359 | Qу |
| 74 | AlaSerProLeuThrIleGluAspGluArgHisIleThrSerValThrAsnLeuLysThr | 721 | Qy |
| 23 | | 2299 | dd |
| 72 | AlaGlySerLeuSerLeuValLeuSerThrCysLysAsnIleTyrSerLeuMetValGlu | 701 | Qy |
| | | 2239 | Db |
| 70 | GlyLysIlePheSerSerAlaThrSerLeuArgLeuGlnIleLysArgCysAlaGlyVal | 681 | Qy |
| 22 | | 2179 | Db |
| 68 | ThrLeuGluValThrLeuArgAspPheSerLysLeuAsnLysGlnAspIleThrTyrLeu | 661 | Qу |
| 21 | | 2119 | Дъ |
| 66 | GluThTTYTIleProSerArgAlaValSerLeuPhePheAsnTrpLysGlnGluPheArg | 641 | ОУ |
| 21 | | 2059 | |
| 64 | MetalaSerTrpGluLysAlaAlaGluAspThrGlyGlyIleHisMetGluGluAlaPro | 621 | Оy |
| 20 | | 1999 | |
| 19 | CATTTGCCCAATTGTGCAAGTGCCCTGGACTTCATTAAACTGGACTTTTATGGGGGAGCT | 1939 | Db |

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Sequence 23, Application US/10221097
GENERAL INFORMATION:
APPLICANT: MAINT Cock, Paul R.
APPLICANT: MINTOCK, Paul R.
APPLICANT: MINTOCK, Paul R.
APPLICANT: MINTOCK, Paul R.
APPLICANT: MINTOCK, Paul R.
APPLICANT: Safia K.
APPLICANT: Stang, Zhaoying
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GP50016
CURRENT APPLICATION NUMBER: US/10/221,097
CURRENT FILING DATE: 2002-09-06
PRIOR APPLICATION NUMBER: FCT/US01/07143
PRIOR FILING DATE: 2000-03-05
PRIOR APPLICATION NUMBER: 60/187,107
PRIOR APPLICATION NUMBER: 60/187,107
PRIOR APPLICATION NUMBER: 60/187,107
PRIOR APPLICATION NUMBER: 60/188,916
PRIOR APPLICATION NUMBER: 60/237,846
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
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PRIOR FILING DATE: 2000-03-13
PRIOR FILING DATE: 2000-10-03
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                      LeuSerAspIleGlyGluGlyMetAspTyrIleValLysSerLeuSerSerGluProCys
                                                                       AsnLeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluGluAspAla
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; TYPE: DNA
; ORGANIAM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (29)..(3226)
PCT-US01-14826-66
                                                                                                                      CURRENT APPLICATION NUMBER: PCT/US01/14826
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/577,408
; PRIOR FILING DATE: 2000-05-18
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; PRIOR APPLICATION NUMBER: 09/775,330<151> 2
; NUMBER OF SEQ ID NOS: 864
; SOFTMARE: Custom
; SEQ ID NO 66
; LENGTH: 3260
 Score:
Percent
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PCT-US01-14826-66
                        Pred.
                                                                                                                                                                                                                                                                                           Sequence 66, Application GENERAL INFORMATION:
                                                                                                                                                                                                                                                          TITLE OF INVENTION: NOVEL NUCLEIC ACIDS FILE REFERENCE: 21272-103
                                                                                                                                                                                                                                                                       APPLICANT: Hyseq, II TITLE OF INVENTION:
                       No . .
                                                                                                                                                                                                                                                                                                                                                                                                                                          3079
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 Similarity
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                                                                                                                                                                                                                                                                                                                                                    CTAGTAACTGCT
                                                                                                                                                                                                                                                                                                                                                             LeuValThrAla
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99.80%
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Length:
Matches:
Conservative:
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2000-10-24
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| Qу Db | Db Qq | Оу | Qу | Qу | Qу | Db Oy | Qу | Db Oy | Db Qy | Db Qy | Qу | Оу | Db 0y | Qy Db | Qy | Оу | US- | Bes |
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| 21 LeuLeuLeuGlnIleGlnLysSerArgCysLeuArgAsnLeuMetLysThrProLeuPhe 340 | 301 ThrGluAspSerAlaGlnAlaLeuIleArgGluValLeuIleLysGluLeuAlaGluGly 320 | 281 ThrGluCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMet 300 | 261 IleGluAlaLeuIleLysGluAsnHisArgPheLysAsnMetValILeValThrThrThr 280 | alLeuPheLeuLeuAspGlyTyrAsnGluPheLysProGlnAsnCysProGlu 2 | 221 LeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLysLeuArg 240 | 201 PhePheLeuArgLeuSerArgAlaGlnGlyGlyLeuPheGluThrLeuCysAspGlnLeu 220 | 181 ArgIleAlaMetLeuTrpGlySerGlyLySCysLysAlaLeuThrLysPheLysPheVal 200 | 161 LeuGlnSerProCysIleIleGluGlyGluSerGlyLysGlyLysSerThrLeuLeuGln 180 | 141 ArgLysAspGlnHisHisHisArgValGluGlnLeuThrLeuAsnGlyLeuLeuGlnAla 160 | 121 GlyGluAspIleAspIleIlePheAsnLeuLysSerThrPheThrGluProValLeuTrp 140 | 101 LeualaGlnäspLeuLysäspLeuTyrHisThrProSerPheLeuäsnPheTyrProLeu 120 | 81 PheGlnAspLeuAsnGlyGlnSerLeuPheHisGlnThrSerGluGlyAspLeuAspAsp 100 | 61 LysGlySerGluSerCysAsnLeuPheLeuLysSerLeuLysGluTrpAsnTyrProLeu 80 | GlyIleIleHisMetIleLe GGGATCATTCACATGATTT | 21 LysGlnIleThrAspAspLeuPheValTrpAsnValLeuAsnArgGluGluValAsnIle 40 | 1 MetAsnPheIleLysAspAsnSerArgAlaLeuIleGlnArgMetGlyMetThrValile 20 ::: | Gaps: x PCT-US01-14826-66 (1-3260) | t Local Similarity: 99.61% Mismatches: 2 ry Match: 99.67% Indels: 0 |
| Qy Db | Qy Db | Qy Db | Qy Db | Qy Db | Qy db | ДУ | Db Qy | da Vy | Db Qy | Qy Db | Db QY | D D | Qy Qy | Qy Db | qa | Db 4 | Db | Qy |
| 681 GlyLysIlePheSerSerAlaThrSerLeuArgLeuGlnIleLysArgCysAlaGlyVal 700 | 661 ThrLeuGluValThrLeuArgAspPheSerLysLeuAsnLysGlnAspIleThrTyrLeu 680 | 641 GluThtTyrIleProSerargAlaValSerLeuPhePheAsnTrpLysGlnGluPheArg [| 2 | 601 1955 | 7 581 GlyLysSerLeuTyrIleAsnSerGlyAsnIleProAspTyrLeuPheAspPhePheGlu 600 | 561 1835 | 541 ThrGluGluGluIleLeuLysalaIleAsnIleAsnSerPheValGluCysGlyIleHis 5 | 1715 | 501 AlaThrArgAlaValMetLysHisLeuAlaAlaValTyrGlnHisGlyCysLeuLeuGly 5 | 481 SeraspileThrSerThrTyrSerSerLeuLeuArgTyrThrCysGlySerSerValGlu 5 | 461 SEPHAGGINFOGLIGGINVALTARILYSGIYASRGJYYTLGUGINLYSMETVALSEFILE 4 | 441 PREPREHISLYSSERPHGGINGIUTYTTIRAIGLYAFQATGLEUISERSERSERLEUILEUTHT 46 | 421 LeuLeuThrThr61yLeuLeuCysLysTyTThrAlaGlnArgPheLysProLysTyrLys 4 | 13 | 1295 | 1235 ACGCTGTTCCATACCTCTGTTGATACAGAAAACAAACAAA | 1175 GTGGTCACCACTTGTGCAATCCAGATGGGTGAAAGTAGTTCCACTCTCACACACA | 341 |

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RESULT 12
US-09-667-298-66
: Sequence 66, Application US/09667298
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
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                                 LeuValThrAla
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                                                                                                                                           AspThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPheGln
                                                                                                                                                          AspLeuGluGluIleGlnLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeu
                                                                                                                                                                                                                                                                                                      GACCTTGAAGAAATTCAATTAGTCTCCTGCTGCTTGTCTGCAAATGCAGTGAAAATCCTA
                                                                                                                                                                                                                                                                                        IleLysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHis
                                                                                                                                      GATACAGAGATTAGAATTTTAGGTGCATTTTTTGGAAAGAACCCTCTGAAAAACTTCCAG
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APPLICANT: Liu, Chenghua
APPLICANT: Zhou, Ping
APPLICANT: Asundi, Vinod
APPLICANT: Ren, Felyan
APPLICANT: Zhao, Qing A.
APPLICANT: Zhao, Qing A.
APPLICANT: Zhao, Qing A.
APPLICANT: Zhang, Jie
APPLICANT: Wang, Jian-Rui
APPLICANT: Wang, Jian-Rui
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: Novel Nucleic Acids
TITLE OF INVENTION: Polypeptides
TILE REFERENCE: 792CIP2A
CURRENT APPLICATION NUMBER: US/09/667,29
CURRENT FILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: 09/577,408
PRIOR TILING DATE: 2000-05-18
NUMBER OF SEQ ID NOS: 178
SOFTWARE: pt_FL_genes Version 2.0
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Best Local Similarity:
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; NAME/KEY: CDS
; LOCATION: (29)..(3229)
US-09-667-298-66
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ORGANISM: Homo
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TH: 3260
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| 540 1774 | 521 LeuSerIleAlaLysArgProLeuTrpArgGlnGluSerLeuGlnSerValLysAsnThr ! | Db Qy |
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| 520 1714 | 501 AlaThrArgAlaValMetLysHisLeuAlaAlaValTyrGlnHisGlyCysLeuLeuGly | ру |
| 500 1654 | 481 SeraspIleThrSerThrTyrSerSerLeuLeuArgTyrThrCysGlySerSerValGlu : | Оу |
| 480 1594 | 461 SerHisGluProGluGluValThrLysGlyAsnGlyTyrLeuGlnLysMetValSerIle (| ОУ |
| 460 1534 | 441 PhePheHisLysSerPheGlnGluTyrThrAlaGlyArgArgLeuSerSerLeuLeuThr | ρb |
| 440 1474 | 421 LeuLeuThrThrGlyLeuLeuCysLysTyrThrAlaGlnArgPheLysProLysTyrLys | DP QA |
| 420 1414 | 401 ValPheSerHisLysPheAspPheGluLeuGlnAspValSerSerValAsnGluAspVal | Оy |
| 400 1354 | 381 ValalaalaSerAspPheIleArgSerLeuAspHisCysGlyAspLeuAlaLeuGluGly | DP PA |
| 380 1294 | 61 ThrLeuPheH1sThrPheTyrAspLeuLeuIleGlnLysAsnLysH1sLysH1sLysGly | ОУ |
| 360 1234 | 341 ValVallleThrCysalalleGlnMetGlyGluSerGluPheHisSerHisThrGlnThr | Фу |
| 340 1174 | 21 LeuLeuLeuGlnIleGlnLysSerArgCysLeuArgAsnLeuMetLysThrProLeuPhe | Qу Дъ |
| 320 1114 | 301 ThrGluAspSerAlaGlnAlaLeuIleArgGluValLeuIleLySGluLeuAlaGluGly | ФФ |
| 300 1054 | 81 ThrGluCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMet | do Qy |
| 280 994 | 261 IleGluAlaLeuIleLysGluAsnHisArgPheLysAsnMetValIleValThrThrThr | ОУ |
| 260 934 | 1 GlnArgValLeuPheLeuLeuAspGlyTyrAsnGluPheLysProGlnAsnCysProGlu | Db Qy |
| 240 874 | 221 LeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLysLeuArg | Qу |
| 220 814 | 201 PhePheLeuArgLeuSerArgAlaGlnGlyGlyLeuPheGluThrLeuCysAspGlnLeu | Оy |
| 200 754 | 181 ArgileAlaMetLeuTrpGlySerGlyLysCysLysAlaLeuThrLysPheLysPheVal | Оy |

| hrgluGlnGlnGluIleLeuLysAlaIleAsnIleAsnSe | CTGATGCTGCCCTGGGGCTGTGACGTGCAAGG GluGluValProGlnLeuValLysLeuGlyLe | 795 CTCA 901 Lysh | Db 2 Qy |
|--|--|--------------------------------|------------|
| 1775 ACTGAGCAAGAATTCTGAAAGCCATAAACATCAATTCTTTTTTTCTTTTTTTT | | 735 GAAA 881 LeuT | |
| 1175 ACTGAGCAAGAATTCTGAAAGCCATAAACATTCAATTC 561 LeuTyrGlnGluSerThrSerLysSerAlaLeuSerGl 1835 TTATATCAAGAGAGTACATCCAATCAAGCCATAAACATCAATTCA 581 GlyLysSerLeuTyrIleAsnSerGlyAsnIleProAs 1895 GGTAAAAGCTTATATATCAAGTGCCCTGAGCCA 581 GlyLysSerLeuTyrIleAsnSerGlyAsnIleProAs 1895 GGTAAAAGCTTATATATCAACTCAGGGAACATCACCCGA 601 HisLeuProAsnCysAlaSerAlaLeuAspTheIleLy 111111111111111111111111111111111111 | LeuHisAsnLeuValLysLeuSerILeLeuAs | 841 AlaG 675 GCTC | |
| 1775 ACTGAGCAAGAATTCTGAAAGCCATAAACATCATTC 561 LeuTyrGlnGluSerThrSerLysSerAlaLeuSerGl | luIleGlnLeuValSerCysCysLeuSe AAATTCAATTAGTCTCCTGCTGCTTGTC | 821 AspI 615 GACC | |
| 1775 ACTGAGCAAGAAATTCTGAAAGCCATAAACATCAATTCO 561 LeuTyrGlnGluSerThrSerLysSerAlaLeuSerGl 1835 TTATATCAAGAAGTCAATTCTGAAAGCCATAAACATCAATTCO 561 LeuTyrGlnGluSerThrSerLysSerAlaLeuSerGl 1835 TTATATCAAGAAGTCAATTCGAAATCAGCCCTGAGCCA 581 GlyLysSerLeuTyrIleAsnSerGlyAsnIleProAs 1895 GGTAAAGCTTATATATCAACTCAGGGAACATCCCCGA 601 HisLeuDroAsnCysAlaSerAlaLeuAspPheIleLy 1995 CATTTGCCCAATTGTGCAAGTGCCCTGGACTCACTCATTA 621 MetAlaSerTrpGluLysAlaAlaGluAspThrGlyGl 1111111111111111111111111111111111 | IleGlyGluGlyMetAspTyrIleValLy ATTGGAGAGGGAATGGATTACATAGTCAA | 801 Leus 555 TTGT | |
| 11111111111111111111111111111111111111 | 31yLeuLysAsnLeuLysLys GCCTGAAAAACCTGAAGAAG | 781 Ile - 495 ATP | |
| 11111111111111111111111111111111111111 | AsnLeuThrLysLeuTleMetAspAsn ACCTTACAAAGCTCATAATGGATAAC | 761 Asr † 435 AAC | |
| 11111111111111111111111111111111111111 | HisAspLeuGlnAsnGlnArgLeuPr | 741 LeuS 375 TTGA | |
| 541 ThrGluGlnGluIleLeuLysAlaIleAsnIleAsnIleAsnIleAsnIleAsnIleAsnIleIllIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII | LeuThrIleGluAspGluArgHisIle | 721 Ala 315 GCC | |
| 541 ThrGluGlnGluIleLeuLysAlaIleAsnIleAsnIleAsnIleAsnIleAsnIleAsnIleAsnIleAsnIleAsnIleAsnIleAsnIleIlli | rLeuSerLeuValLeuSerThrCysLysAs CTCAGTTTGGTCCTCAGCACCTGTAAGAA | 701 Alac 255 GCTC | |
| 541 ThrGluGlnGluIleLeuLysAlaIleAsnIleAsnIleAsnIleAsnIleAsnIleIllIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII | SerSerAlaThrSerLeuAr | 681 GLy 195 GGG | |
| 541 ThrGluGlnGluIleLeuLysAlaIleAsnIleAsnIleAsnIleAsnIleAsnIleAsnIleAsnIleAsnIleAsnIleAsnIleAsnIleIllIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII | JArgAspPheSerLysLeuAs | 661 Thri | |
| 541 ThrGluGlnGluIleLeuLysAlaIleAsnIleAsnIleAsnIleAsnIleAsnIleAsnIleAsnIleAsnIleAsnIleAsnIleAsnIleIllIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII | IleProSerArgAlaValSerLeuPhe | 641 GluT 075 GAAA | |
| 541 ThrGluGlnGluIleLeuLysAlaIleAsnIleAsnIleAsnIleAsnIleAsnIleAsnIleAsnIleAsnIleAsnIleAsnIleAsnIleAsnIleIllIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII | rpGluLysAlaAlaGluAspThrGl | 621 Met 015 ATG | |
| 541 ThrGluGlnGluIleLeuLysAlaIleAsnIleAsnIleAsnIleAsnIleAsnIleAsnIleAsnIleAsnIleAsnIleAsnIleAsnIleAsnIleIllIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII | OASnCysAlaSerAlaLe | 01 His 55 CAT | Qу Бъ 1 |
| 541 ThrGluGlnGluIleLeuLysAlaIleAsnIleAsn | LeuTyrIleAsnSerGlyAsnI] TTATATATCAACTCAGGGAACA | 81 Gly 95 GGT | Qy Db 1 |
| 541 ThrGluGlnGluIleLeuLysAlaIleAsnIleAsn | luSerThrSerLysSerAlaLeuSer | 61 LeuT 35 TTAT | Qy Db 1 |
| | GluīleLeuLysAlaīleAsnīleAs | 541 Thr 775 ACT | |

| Qy | Query DB: US-09: | Aligna Pred. Score: Percen | ; ; US-I | | S | | | | | | RESULT US-09- ; Sequ | Db Qy | Ωу | QУ | Ф | оу Об | Db Qy | Db |
|--|---|--|--|--|--|---|--|--|--|--------------------------------------|---|----------------------------|--|---|--|--|--|-----|
| 1 MetAsnPheIleLysAspAsnSerArgAlaLeuI | Match: 99.628 Index: 99.628 Gaps: 33 Gaps: 697-089-2 (1-1024) x US-09-864-921-96 (1-3396) | NO: SCORES: 0 5438.00 | NAME/KEY: CDS LOCATION: (277)(3348) 09-864-921-96 | TYPE: DNA ORGANISM: Homo sapien FEATURE: | F SEQ ID NO: FastSEQ f | PRIOR APPLICATION NUMBER: US 09/686,347 PRIOR FILING DATE: 2000-10-10 PRIOR FILING DATE: 2000-10-10 PRIOR APPLICATION NUMBER: US 60/275,980 PRIOR FILING DATE: 2001-03-14 | URRENT APPLICATION NUMBER: US/09/864,921 URRENT FILING DATE: 2001-05-23 FIOR APPLICATION NUMBER: US 09/579,240 | ; APPLICANT: Hayash, Higeki ; APPLICANT: Paulowski, Krzysztof ; TITLE OF INVENTION: Novel Card Domain Containing ; TITLE OF INVENTION: Polypeptides, Encoding Nucleic Acids, and Methods of Use | APPLICANY: STENILK, CHRISTIAN APPLICANT: Damiano, Jason S. APPLICANT: Lee, Sug-Hyung APPLICANT: Oliveira, Vasco A. | Reed, John Pio, Fred Godzik, P | SULT 13 -09-864-921-96 Sequence 96, Application US/09864921 | 1021 LeuvalThrAla 1024 | 1001 ArgLeuValGlyTrpGlnPheAspAspAspAspLeuSerValIleThrGlyAlaPheLys 1020 | 981 ProAlaLeuValargLysLeuSerGlnValLeuSexLysLeuThrPheLeuGlnGluAla 1000 | 961 PheGluAsnLeuLysGlnLeuValPhePheAspPheSerThrLysGluPheLeuProAsp 980 | 941 GlnLeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTrpLeuAlaPheMetGlyVal 960 | 921 ASPThrGluIleArgIleLeuGlyAlaPhePheGlyLySASnProLeuLySASnPheGln 940 | |
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| 361 ThrLeuPheHisThrPheTyrAspLeuLeuIleGln | | 321 LeuLeuLeuGlnIleGlnLysSerArgCysLeuArgAsnLeuMetLysThrProLeuPhe | 301 ThrGluAspSerAlaGlnAlaLeuIleArgGluValLeuIleLysGluLeuAlaGluGly | 281 ThrGluCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMet | 261 IleGluAlaLeuIleLysGluAsnHisArgPheLysAsnMetValIleValThrThrThr | 241 GlnAr 997 CAGAG | 221 1 937 (| 201 877 | 181 817 | 161 757 | 141 697 | 121 637 | 101 577 | 81 517 | 61 457 | 41 397 | 21 337 | 277 |

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Sequence 1319, Application US/09491404
; GENERAL INFORMATION:
APPLICANT: Tang, Yuanhua T.
APPLICANT: Tillinghast, John
; APPLICANT: Sinku, Ankura
; APPLICANT: Liu, Chenghua
; APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: Novel Contigs Obtained
; TITLE OF INVENTION: From Various Libraries
; FILE REFERENCE: 785
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/491,404
CURRENT FILING DATE: 2000-01-27
NUMBER OF SEQ ID NOS: 3796
SOFTWARE: pt_SP_genes Version 1.0
SEQ ID NO 1319
LENGTH: 3545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: sig_peptide
LOCATION: (781)...(916)
OTHER INFORMATION: this location contains the signal peptide sequence,
OTHER INFORMATION: MLMGSGKCKALTKFKEVFFLRLSRAQGGLFETLCDQLLDIPGTIR, Run
FEATURE:
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LOCATION: (679)...(3279)
OTHER INFORMATION: similar to gi3688110 in
OTHER INFORMATION: Run with FASTXY 3.3t00,
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| i io | CTGAGCAAGAATTCTGAAAGCCATAAACATCAATTCCTTTGTAGAGTGTGGCATCCAT | ເກ | Db |
| 560 | ThrGluGluGluIleLeuLysAlaIleAsnIleAsnSerPheValGluCysGlyIleHis | | Qу |
| 540 | LeuSerIleAlaLysArgProLeuTrpArgGlnGluSerLeuGlnSerValLysAsnThr | 521 | Qy |
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| 460 | PhePheHisLysSerPheGlnGluTyrThrAlaGlyArgArgLeuSerSerLeuLeuThr | 441 | Qy |
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| 440 1551 | LeuLeuThrThrGlyLeuLeuCysLysTyrThrAlaGlnArgPheLysProLysTyrLys | 21 92 | Qy |
| 420 | ValPheSerHisLysPheAspPheGluLeuGlnAspValSerSerValAsnGluAspVal | 401 | Qy |
| 1491 | | 1432 | Db |
| 400 | ValalaalaSerAspPheIleArgSerLeuAspHisCysGlyAspLeuAlaLeuGluGly | 381 | Qy |
| 1431 | | 1372 | Db |
| 380 | ThrLeuPheHisThrPheTyrAspLeuLeuIleGlnLysAsnLysHisLysHisLysGly | 361 | Qy |
| 1371 | | 1312 | Db |
| 360 | ValValIleThrCysAlaIleGlnMetGlyGluSerGluPheHisSerHisThrGlnThr | 341 | Qy |
| 1311 | | 1252 | Db |
| 340 | LeuLeuGlnİleGlnLysSerArgCysLeuArgAsnLeuMetLysThrProLeuPhe | 321 | Qy |
| 1251 | | 1192 | Db |
| 320 | ThrGluAspSerAlaGlnAlaLeuIleArgGluValLeuIleLysGluLeuAlaGluGly | 301 | Qy |
| 1191 | | 1132 | Db |
| 300 | ThrGluCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMet | 281 | Qy |
| 1131 | | 1072 | Db |
| 280 | IleGluAlaLeuIleLysGluAsnHisArgPheLysAsnMetVallleValThrThrThr | 261 | Qy |
| 1071 | | 1012 | Db |
| 260 | GlnArgValLeuPheLeuLeuAspGlyTyrAsnGluPheLysProGlnAsnCysProGlu | 241 | Qy |
| 1011 | | 952 | Db |
| 240 | LeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLysLeuArg | 221 | Qy |
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                                                                                    LeuThrAlaLeuMetLeuProTrpGlyCysAspValGlnGlySerLeuSerSerLeuLeu
                                                                                                          AlaGlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeu
                                                                                                                                                                      AlaGlySerLeuSerLeuValLeuSerThrCysLysAsnIleTyrSerLeuMetValGlu
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                                                      LysHisLeuGluGluValProGlnLeuValLysLeuGlyLeuLysAsnTrpArgLeuThr
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               GATACAGAGATTAGAATTTTAGGTGCATTTTTTGGAAAGAACCCTCTGAAAAACTTCCAG
                                             AAACATTTGGAGGAGGTCCCACAACTCGTCAAGCTTGGGTTGAAAAACTGGAGACTCACA
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CURRENT APPLICATION NUMBER: US/09/922,27
CURRENT FILING DATE: 2001-08-03
PRIOR APPLICATION NUMBER: 09/491,404
PRIOR FILING DATE: 2001-01-25
NUMBER OF SEQ ID NOS: 3796
SOFTWARE: pt_SP_genes Version 1.0
SEQ ID NO 1319
LENGTH: 3545
                                                                                                                                                                                                                                                                                                        FEATURE:

NAME/KEY: sig_peptide

LOCATION: (781)...(916)

OTHER INFORMATION: this location contains the signal peptide sequence,

OTHER INFORMATION: MLWGSGKCKALTKFKFVFFLRLSRAQGGLFETLCDQLLDIPGTIR, Run

NAME/KEY: misc_feature

LOCATION: (679)...(3279)

OTHER INFORMATION: similar to gi3688110 in the genepept database relea

OTHER INFORMATION: Run with FASTXX 3.3t00, default parameters

US-09-922-279-1319
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Sinku, Ankura
APPLICANT: Liu, Chenghua
APPLICANT: DIMANAC, Radoje T.
TITLE OF INVENTION: Novel Contigs Obtained
TITLE OF INVENTION: From Various Libraries
FILE REFERENCE: 785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Tang, Yuanhua APPLICANT: Tillinghast,
                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo
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| ob Dy | 61 412 | LysGlySerGluSerCysAsnLeuPheLeuLysSerLeuLysGluTrpAsnTyrProLeu 8 | 0 71 |
|------------------|-------------|---|-----------|
| 3 5 | 81 | snGlyGlnSerLeuPheHisGlnThrSerGluGlyAspLeuAspAsp 1 | 00 |
| Ωy | 101 | euAlaGlnAspLeuLysAspLeuTyrHisThrProSerPheLeuAsnPheTyrProLeu 1 | 20 |
| 용 | 532 | TGGCTCAGGATTTAAAGGACTTGTACCATACCCCATCTTTTCTGAACTTTTATCCCCTT 5 | 91 |
| V 0 | 121 | GlyGluAspIleAspIleIlePheAsnLeuLysSerThrPheThrGluProValLeuTrp | 40 |
| > | 141 | gLvsAspGlnHisHisArgValGlnGlnLenThrLenAspGlvLenLenGlnAla 1 | 90 H |
| 용 : | 652 | AGGAAGGACCAACACCATCACCGGTGGAGCAGCTGACCCTGAATGGCCTCCTGCAGGCT 7 | |
| Σ¥ | 161 | GeuGln 1 | 80 |
| A | 712 | TTCAGAGCCCCTGCATCATTGAAGGGGAATCTGGCAAAGGCAAGTCCACTCTGCTGCAG 7 | 71 |
| Ą | 181 | ysCysLysAlaLeuThrLysPheLysPheVal 2 | |
| 9 | 772 | GCATTGCCATGCTCTGGGGCTCCGGAAAGTGCAAGGCTCTGACCAAGTTCAAATTCGTC 8 | 31 |
| 8 8 | 201 832 | PhePheLeuArgLeuSerArgAlaGlnGlyGlyLeuPheGluThrLeuCysAspGlnLeu 2 | 20 91 |
| Ŋ | 221 | euAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLysLeuArg 2 | 40 |
| В | 892 | TGGATATACCTGGCACAATCAGGAAGCAGACATTCATGGCCATGCTGCTGAAGCTGCGG | 51 |
| д ₂ у | 241 952 | <pre>snGluPheLysProGlnAsnCysProGlu 2 </pre> | 011 |
| ν | 261 | neLysAsnMetValIleValThrThrThr 2 | 80 |
| В | 1012 | TCGAAGCCCTGATAAAGGAAAACCACCGCTTCAAGAACATGGTCATCGTCACCACTACC 1 | 071 |
| Ϋ́O | 281 | | 00 |
| , 8 | Z/07 | CTGAGTGCCTGAGGCACATACGGCAGTTTGGTGCCCTGACTGCTGAGGTGGGGGATATG 1 | 131 |
| β 2 γ | 301 1132 | uValLeuIleLysGluLeuAlaGluGly 3 | 191 |
| ł ń | 321 | PuArgAsnLeuMetLysThrProLeuPhe 3 | 2 0 |
| У | 341 | alValIleThrCysAlaIleGlnMetGlyGluSerGluPheHisSerHisThrGlnThr 3 | 60 |
| 岁 | 1252 | GTCATCACTTGTGCAATCCAGATGGGTGAAAGTGAGTTCCACTCTCACACACA | 311 |
| ₽ ¾ | 361 1312 | ThrLeuPheHisThrPheTyrAspLeuLeuIleGlnLysAsnLysHisLysHisLysGly 3 | 80 371 |
| 8 8 | 381 1372 | ValalaalaseraspPheIleargSerLeuaspHisCysGlyaspLeualaLeuGluGly 4 | 00 |
| Ϋ́ | 401 | ValPheSerHisLysPheAspPheGluLeuGlnAspValSerSerValAsnGluAspVal 4 | 20 |
| 岁 | w | TGTTCTCCCACAAGTTTGATTTCGAACTGCAGGATGTGTCCAGCGTGAATGAGGATGTC 1 | 491 |

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              LeuSerAspIleGlyGluGlyMetAspTyrIleValLysSerLeuSerSerGluProCys
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Search completed: January 31, 2003, 13:16:41 Job time: 5276 secs

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Command line parameters:

MODEL-frame+_p2n.model -DEV-xlh
-Q-/Gqn2_1/USPTO_Spool_VG09697089_runat_29012003_092506_19212/app_query.fasta_1.1223
-Q-/Gqn2_1/USPTO_Spool_VG09697089_runat_29012003_092506_19212/app_query.fasta_1.1223
-DB=Pending_Patents_NA_New -QFMT-fastap -SUFFIX=p2n.rnpn -MINMATCH=0.1
-LOOPCIL=0 -LOOPEXY=0 -UNITS=011ts -START=1 -END--1 -MATRIX-pam120
-TRANS-human40.cd1 -LISTS=011ts -START=1 -END--1 -THR_XCORE-pct -THR_XX=100
-THR_XNIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT-pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER-US09697089_eCGN_1 = 1114_erunat_29012003_092506_19212
-NCPU=6 -ICPU=3 -NO_XLDX -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -MAIT -LONGLOG
-DEV_TIMEDUT=120 -WARN_TIMEDUT=30 -THREADS=1 -XGAPOP=4 -XGAPEXT=12 -FGAPOP=6
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Listing first 45 summaries
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US-10-285-408-2
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1, Appli
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| 3101, 3981, 19376, | 6799, 6799, 6806, 6806, 6808, | equence 6807, equence 6817, equence 6817, equence 6809, equence 6809, equence 6809, equence 6797, | nce 6818, nce 6798, nce 6800, nce 6800, nce 6815, nce 6815, | Sequence 6819, Ap Sequence 6801, Ap Sequence 6801, Ap Sequence 6810, Ap Sequence 6810, Ap Sequence 6816, Ap Sequence 6824, Ap Sequence 6824, Ap |

ALIGNMENTS

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| 380 1140 | ThrLeuPheHisThrPheTyrAspLeuLeuIleGlnLysAsnLysHisLysHisLysGly | 361 1081 | Db 99 |
|-------------|--|-------------|-------|
| 360 1080 | ValValIleThrCysAlaIleGlnMetGlyGluSerGluPheHisSerHisThrGlnThr | 341 1021 | рь |
| 340 1020 | LeuLeuLeuGlnIleGlnLysSerArgCysLeuArgAsnLeuMetLysThrProLeuPhe | 321 961 | Ф |
| 320 960 | laGlnAlaLeuIleArgGluValLeuIleLy | | рь |
| 300 | ThrGluCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGlu | | Db Qy |
| 280 840 | l IleGluAlaLeuIleLysGluAsnHisArgPheLysAsnMetValIleValThrThrThr | 26 78 | D 04 |
| 260 780 | GlnArgValLeuPheLeuLeuAspGlyTyrAsnGluPheLysProGlnAsnCysProGlu | 24 72 | DP QA |
| 240 720 | euAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLysLeuA | | Оу |
| 220 | PhePheLeuArgLeuSerArgAlaGlnGlyGlyLeuPheGluThrLeuCysAspGlnL | | 당 왕 |
| 200 | ArgIleAlaMetLeuTrpGlySerGlyLySCYsLySAlaLeuThrLysPheLysP | 4- 00 | pb 09 |
| 180 540 | LeuGlnSerProCysIleIleGluGlyGluSerGlyLySGlyLySSerThrLeuLeuGln | 161 481 | Дb |
| 160 480 | ArgLysAspGlnHisHisHisArgValo | | dp da |
| 140 420 | G1yG1uAspI1eAspI1eI1ePheAsnLeuLysSerThrPheThrG1uPr | 121 361 | Db Qy |
| 120 360 | L LeuAlaGlnAspLeuLysAspLeuTyrHisThrProSerPheLeuAsnPheTyrProLeu | 30: | р |
| 300 | PheGlnAspLeuAsnGlyGlnSerLeuPheHisGlnThrSerGluGlyAspLeuAspAsp | 81 241 | Ф |
| 80 240 | L LysGlySerGluSerCysAsnLeuPheLeuLysSerLeuLysGluTrpAsnTyrProLeu | 61 181 | Оу |
| 60 180 | IleCysCysGluLysValGluGlnAspAlaAlaArgGlyIleIleHisMetIleLeuLys | 41 121 | Оy |
| 40 120 | LysGlnIleThrAspAspLeuPheValTrpAsnValLeuAsnArgGluGluValAsnIle | 6 2 | ф |

| 760 | LeuSerIleHis AspLeuGlnAsnGlnArgLeuProGlyGlyLeuThrAspSerLeuGly | 741 | Qy |
|------|--|------|----------|
| 2220 | CTGTAACAAACCTGAAA | 2161 | Db |
| 740 | laSerProLeuThrIleGluAspGluArgHisIleThrSerValThrAsnLeuLysTh | 721 | Qy |
| 2160 | AAGCCTCAGTTTGGTCCTCAGCACCTGTAAGAACATTTATTCTCTCATGGTG | 2101 | ДĎ |
| 720 | .laGlySerLeuSerLeuValLeuSerThrCysLysAsnIleTyrSerL | 701 | γо |
| 2100 | GGAAAATATTCAGCTCTGCCACAAGCCTCAGGCTGCAAATAAAGAGATGTGCTGGTGTG | 2041 | дb |
| 700 | lyLysIlePheSerSerAlaThrSerLeuArgLeuGlnIleLysArgCysAlaGlyV | 681 | Qy |
| 2040 | G | 1981 | Db |
| 680 | hrLeuGluValThrLeuArgAspPheSerLysLeuAsnLysGlnAspIleThrT | 661 | ду |
| 1980 | GAAACCTACATTCCCAGCAGGGCTGTATCTTTGTTCTTCAACTGGAAGCAGGAATTCAGG | 1921 | ФФ |
| 660 | ${\tt luThrTyrIleProSerArgAlaValSerLeuPhePheAsnTrpLysGlnGluPheAr}$ | 641 | ΩУ |
| 1920 | ATGGCTTCATGGGAAAAGGCTGCAGAAGACACAGGTGGAATCCACATGGAAGAGGCCCCA | 1861 | Db |
| 640 | etAlaSerTrpGluLysAlaAlaGluAspThrGlyGlyIleHisMetGluGluAlaPr | 621 | ОУ |
| 1860 | CATTTGCCCCAATTGTGCAAGTGCCCTGGACTTCATTAAACTGGACTTTTATGGGGGAGCT | 1801 | ρb |
| 620 | isLeuProAsnCysAlaSerAlaLeuAspPheIleLysLeuAspPheTyrGlyGlyA | 601 | ур |
| 1800 | GTAAAAGCTTATATATCAACTCAGGGAACATCCCCGATTACTTATTTGACTTCTTTGAA | 1741 | ДĎ |
| 600 | lyLysSerLeuTyrIleAsnSerGlyAsnIleProAspTyrLeuPheAspPhePheC | 581 | ОУ |
| 1740 | TTATATCAAGAGTACATCCAAATCAGCCCTGAGCCAAGAATTTGAAGCTTTCTTT | 1681 | ф |
| 580 | euTyrGlnGluSerThrSerLysSerAlaLeuSerGlnGluPheGluAlaPhePheG | 561 | Qy |
| 1680 | ACTGAGCAAGAATTCTGAAAGCCATAAACATCAATTCCTTTGTAGAGTGTGGCATCCAT | 1621 | ДЪ |
| 560 | hrGluGlnGluIleLeuLysAlaIleAsnIleAsnSerPheValGluCysGlyIleHi | 541 | уо |
| 1620 | CTTTCCATCGCCAAGAGGCCTCTCTGGAGACAGGAATCTTTGCAAAGTGTGAAAAACACC | 1561 | дд |
| 540 | euSerIleAlaLysArgProLeuTrpArgGlnGluSerLeuGlnSerValLysAs | 521 | уо |
| 1560 | GCCACCAGGCTGTTATGAAGCACCTCGCAGCAGTGTATCAACACGGCTGCCTTCTCGGA | 1501 | Db |
| 520 | laThrArgAlaValMetLysHisLeuAlaAlaValTyrGlnHisGlyCysLeuLeuG | 501 | Qγ |
| 1500 | TCGGACATTACATCCACTTATAGCAGCCTGCTCCGGTACACCTGTGGGTCATCTGTGGAA | 1441 | Db |
| 500 | erAspIleThrSerThrTyrSerSerLeuLeuArgTyrThrCysGlySerSerValC | 481 | Qy |
| 1440 | | 1381 | Db |
| 480 | erHisGluProGluGluValThrLysGlyAsnGlyTyrLeuGlnLysMetValSerIl | 461 | VQ VQ |
| 1380 | TTCTTTCACAAGTCATTCCAGGAGTACACAGCAGGACGAGCTCAGCAGTTTATTGACG | 1321 | Db |
| 460 | hePheHisLysSerPheGlnGluTyrThrAlaGlyArgArgLeuSerSerLeuLeuI | 441 | VQ |
| 1320 | CTGCTGACAACTGGGCTCCTCTGTAAATATACAGCTCAAAGGTTCAAGCCAAAGTATAAA | 1261 | Db |
| 440 | euLeuThrThrGlyLeuLeuCysLysTyrThrAlaGlnArgPheLysProLysTyr | 421 | Qy |
| 1260 | GTGTTCTCCCACAAGTTTGATTTCGAACTGCAGGATGTGTCCAGCGTGAATGAGGATGTC | 1201 | Db |
| 420 | alPheSerHisLysPheAspPheGluLeuGlnAspValSerSerValAsnGluAspV | 401 | Qy |
| 1200 | GTGGCTGCAAGTGACTTCATTCGGAGCCTGGACCACTGTGGAGACCTAGCTCTGGAGGGT | 1141 | ДĎ |
| 400 | alAlaAlaSerAspPheIleArgSerLeuAspHisCysGlyAspLeuAlaLeuGluGl | 381 | Qy |
| | | | |

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Sequence 14, Application PC/TUS0221946A
GENERAL INFORMATION:
APPLICANT: Thomas Jefferson University
APPLICANT: Alnemri, Emad S.
TITLE OF INVENTION: IPAF, AN ICE-PROTEASE AC
TITLE OF INVENTION: FACTOR
FILLE REPERENCE: 480140, 47PC
CURRENT APPLICATION NUMBER: PCT/US02/21946A
CURRENT FILING DATE: 2002-05-24
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 14
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                                                                                                                                                               ArgLeuValGlyTrpGlnPheAspAspAspAspLeuSerValIleThrGlyAlaPheLys
                                                                                                                                                                                                                                          PheGluAsnLeuLysGlnLeuValPhePheAspPheSerThrLysGluPheLeuProAsp
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                                                         LysGlnIleThrAspAspLeuPheValTrpAsnValLeuAsnArgGluGluValAsnIle
                        ArgilealaMetLeuTrpGlySerGlyLysCysLysAlaLeuThrLysPheLysPheVal
                                                                                                                                                                                                        LeuGlnSerProCysIleIleGluGlyGluSerGlyLysGlyLysSerThrLeuLeuGln
                                                                                                                                                                                                                                                                           GlyGluAspIleAspIleIlePheAsnLeuLysSerThrPheThrGluProValLeuTrp
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| 660 2124 | 641 GluThrTyrIleProSerArgAlaValSerLeuPhePheAsnTrpLysGlnGluPheArg | Qу |
|-------------|--|----------|
| 640 2064 | 21 MetAlaSerTrpGluLysAlaAlaGluAspThrGlyGlyIleHisMetGluGluAlaPro | Оу |
| 620 2004 | 01 HisLeuProAsnCysalaSerAlaLeuAspPheIleLysLeuAspPheTyrGlyGlyAla | Qу рь |
| 600 1944 | 581 GlyLysSerLeuTyrIleAsnSerGlyAsnIleProAspTyrLeuPheAspPhePheGlu | Оу |
| 580 1884 | 561 LeuTyrGlnGluSerThrSerLysSerAlaLeuSerGlnGluPheGluAlaPhePheGln | Db Qy |
| 560 1824 | 541 ThrGluGlnGluIleLeuLysalaIleAsnIleAsnSerPheValGluCysGlyIleHis | Оy |
| 540 1764 | 21 LeuSerIlealaLysArgProLeuTrpArgGlnGluSerLeuGlnSerValLysAsnThr | Оy |
| 520 1704 | 01 AlaThrArgAlaValMetLysHisLeuAlaAlaValTyrGlnHisGlyCysLeuLeuGly | Оу |
| 500 1644 | 81 SeraspileThrSerThrTyrSerSerLeuLeuArgTyrThrCysGlySerSerValGlu | Db Qy |
| 480 1584 | 461 SerHisGluProGluGluValThrLysGlyAsnGlyTyrLeuGlnLysMetValSerIle | Qу Дъ |
| 460 1524 | 41 PhePheHisLysSerPheGlnGluTyrThrAlaGlyArgArgLeuSerSerLeuLeuThr | ФФ |
| 440 1464 | 421 LeuLeuThrThrGlyLeuLeuCysLysTyrThrAlaGlnArgPheLysProLysTyrLys | QУ |
| 420 1404 | 401 ValPheSerHisLysPheAspPheGluLeuGlnAspValSerSerValAsnGluAspVal | Db Qy |
| 400 1344 | 381 ValAlaAlaSerAspPheIleArgSerLeuAspHisCysGlyAspLeuAlaLeuGluGly | Db Qq |
| 380 1284 | 361 ThrLeuPheHisThrPheTyrAspLeuLeuIleGlnLysAsnLysHisLysHisLysGly | Оу |
| 360 1224 | 41 ValVallleThrCysAlaIleGlnMetGlyGluSerGluPheHisSerHisThrGlnThr | ОУ |
| 340 1164 | 21 LeuLeuLeuGlnIleGlnLysSerArgCysLeuArgAsnLeuMetLysThrProLeuPhe | Db Db |
| 320 1104 | 301 ThrGluAspSerAlaGlnAlaLeuIleArgGluValLeuIleLysGluLeuAlaGluGly : | Оу |
| 1044 | 985 ACTGAGTGCCTGAGGCACATACGGCAGTTTGGTGCCCTGACTGCTGAGGTGGGGGATATG | ф |

| 3204 | GGCTTGTTGGGTGGCAATTTGATGATGATGATCTCAGTGTTATTACAGGTGCTTTTAA | 14 | Db |
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| 1020 | Arc | Ó | Qy |
| - | CCAGCATTAGTCAGAAAACTTAGCCAAGTGTTATCCAAGTTAACTTTTCTGCAAGAAGCT | oo o | Db 45 |
| 1000 | ProAlaLeuValArgLvsLeuSerGlnValLeuSerLvsLeuThrPheLeuGlnGluAla | 98 | 0Δ |
| 3084 | PheGluAsnLeuLysGlnLeuValPhePheAspPheSerThrLysGluPheLeuProAsp | 96: 302: | DP QV |
| | CAGTTGAATTTGGCGGGAAATCGTGTGAGCAGTGATGGATG | σ | מנו |
| 960 | GlnLeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTrpLeuAlaPheMetGlyVal | 94 | , Q |
| 2964 | S GATACAGAGATTTAGGATTTTAGGTGCATTTTTTTGGAAAGAACCCTCTGAAAAACTTCCAG | 290 | Db |
| 940 | AspThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPheGln | 921 | Qy |
| 2904 | AAACATTTGGAGGAGGTCCCACAACTCGTCAAGCTTGGGTTGAAAAACTGGAGACTCACA | 2845 | Дb |
| 920 | LeuGluGluValProGlnLeuValLysLeuGlyLeuLysAsnTrpArgLeuThr | 90: | Qy |
| 2844 | 5 CTCACCGCACTGATGCTGCCCTGGGGCTGTGACGTGCAAGGCAGCCTGAGCAGCCTGTTG | 2785 | 망 |
| 900 | LeuThrAlaLeuMetLeuProTrpGlyCysAspValGlnGlySerLeuSerSerLeuLeu | 881 | Qy |
| 2784 | | 2725 | фd |
| 880 | luLysAspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGluGln | 861 | Qγ |
| 2724 | GCTCAGAATCTTCACAATTTGGTCAAACTGAGCATTCTTGATTTATCAGAAAATTACCTG | 2665 | 망 |
| 860 | AlaGlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeu | 841 | Qy |
| 2664 | GACCTTGAAGAAATTCAATTAGTCTCCTGCTGCTGCTGCTGCAAATGCAGTGAAAATCCTA | 2605 | ДЬ |
| 840 | AspLeuGluGluIleGlnLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeu | 821 | Qy |
| | | | Db |
| 820 | rAspIleGlyGluGlyMetAspTyrIleValLysSerLeuSerSerGluProCys | ω | 0 ν |
| 2544 | | 8 | Db |
| 800 | IleLysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHis | 781 | γΩ |
| 2484 | AACTTGAAGAACCTTACAAAGCTCATAATGGATAACATAAAGATGAATGA | 2425 | Db |
| 780 | AsnLeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluGluAspAla | 761 | Qy |
| 2424 | | œ. | Db - |
| 760 | LeuSerIleHisAspLeuGlnAsnGlnArgLeuProGlyGlyLeuThrAspSerLeuGly | 741 | Qy |
| 2364 | GCCAGTCCCCTCACCATAGAAGATGAGAGGCACATCACATCTGTAACAAACCTGAAAAACC | 2305 | Db |
| 740 | AlaSerProLeuThrIleGluAspGluArgHisIleThrSerValThrAsnLeuLysThr | 721 | Qy |
| 2304 | GCTGGAAGCCTCAGTTTGGTCCTCAGCACCTGTAAGAACATTTATTCTCTCATGGTGGAA | 2245 | Db |
| 720 | AlaGlySerLeuSerLeuValLeuSerThrCysLysAsnIleTyrSerLeuMetValGlu | 701 | Qy |
| 2244 | GGGAAAATATTCAGCTCTGCCACAAGCCTCAGGCTGCAAATAAAGAGATGTGCTGGTGTG | 2185 | Db |
| 700 | GlyLysIlePheSerSerAlaThrSerLeuArgLeuGlnIleLysArgCysAlaGlyVal | 681 | Qy |
| 2184 | ACTCTGGAGGTCACACTCCGGGATTTCAGCAAGTTGAATAAGCAAGATATCAGATATCTG | 2125 | Db |
| 680 | hrLeuGluValThrLeuArgAspPheSerLysLeuAsnLysGlnAspIleThrTyrLeu | 661 | Оу |

```
RESULT 3
US-10-276-781-111
Sequence 111, Application US/10276781
Sequence 111, Application US/10276781
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
APPLICANT: Tang et al.
TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
FILE REFERENCE: 21272-018 (785 contig)
CURRENT APPLICATION NUMBER: US/10/276,781
CURRENT FILING DATE: 2002-11-18
PRIOR APPLICATION NUMBER: 09/491,404
PRIOR APPLICATION NUMBER: 09/491,404
PRIOR FILING DATE: 2000-01-25
NUMBER OF SEQ ID NOS: 2018
SOFTWARE: FASTSEQ for Windows Version 3.0
FORTH: 3548
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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; TYPE: DNA
; ORGANISM: HOMO S
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| Qy 341 Db 1252 |
| Qy 321 Db 1192 |
| Qy 301 Db 1132 |
| Qy 281 Db 1072 |
| Qy 261 Db 1012 |
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| Qy 221 Db 892 |
| Qy 201 Db 832 |

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AspThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPheGln
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TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACII
TITLE OF INVENTION: ANALYSIS OF GENE EXPRESSION IN BT 474
FILE REFERENCE: PB 0004 WO 8
CURRENT APPLICATION NUMBER: US/10/203,138A
CURRENT FILING DATE: 2002-08-02
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 04 February 2000 (04.02.00)
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 05 May 2000 (26.05.00)
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 03 August 2000 (03.08.00)
PRIOR PRIOR FILING DATE: 03 October 2000 (03.10.00)
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 03 October 2000 (07.09.00)
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: US 60/236,369
PRIOR APPLICATION NUMBER: US 60/236,687
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 21 September 2000 (30.06.00)
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 30 June 2000 (30.06.00)
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                                                  Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                               ; OTHER INFORMATION: US-10-203-138A-4307
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US-09-697-089-2
                                                                                                        Score:
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SOFTWARE: Molecular Dynamics Sequence Listing
SEQ ID NO 4307
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CURRENT APPLICATION NUMBER: US/10/203,138A
CURRENT EILING DATE: 2002-08-02
PRIOR PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 04 February 2000 (04.02.00)
PRIOR PRIOR PRIOR DATE: 04 February 2000 (24.02.00)
PRIOR PRIOR PRIOR DATE: 26 May 2000 (26.05.00)
PRIOR PRIOR FILING DATE: 26 May 2000 (26.05.00)
PRIOR FILING DATE: 03 August 2000 (03.08.00)
PRIOR PRIOR FILING DATE: 03 August 2000 (03.08.00)
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 27 September 2000 (27.09.00)
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 21 September 2000 (21.09.00)
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 21 September 2000 (21.09.00)
PRIOR APPLICATION NUMBER: US 60/268,408
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                                                                                                                Best Local Similarity:
Query Match:
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                                                                                                                                                            Percent Similarity:
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SOFTWARE: Molecular Dynamics Sequence Listing SEQ ID NO 9429
LENGTH: 220
TYPE: DNA
ORGANIC:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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OTHER INFORMATION: MAP TO AC011232.3
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944 LeuAlaGlyAsnArgValSerSerAspGlyTrpLeuAlaPheMetGlyValPheGluAsn 963
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Chen, Wensheng
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Rank, David R
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Best Local Similarity:
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LENGTH: 5984
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APPLICANT: IKEDA, Johe
APPLICANT: SAKAI, Harumi
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                            AspGlyTyrAsnGluPheLysProGlnAsnCysProGluIleGluAlaLeuIleLysGlu
                                                                                                                                    TGCTGTCCCCTGTTAAACAGGTTCCAGCTGGTTTTCTACCTCTCCCTTAGTTCCACCAGA 1821
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Sequence 84, Application US/09949002

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METH
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL000790

CURRENT APPLICATION NUMBER: US/09/949,002

CURRENT FILING DATE: 2000-01-28

PRIOR APPLICATION NUMBER: 60/231,401

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 10823
   ; TYPE: DNA
; ORGANISM: Human
US-09-949-002-84
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                                             CATGTGCTTGATGAGCAAATTTACAGCCCAGAGACTAAGACCATTCTACCGGTTTTTAAG
                                                           rThrGlyLeuLeuCysLysTyrThrAlaGlnArgPheLysProLysTyrLysPhePheHi
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US-09-697-089-2 (1-1024) x US-09-949-002-84 (1-6133)
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TGCTGTCCCCTGTTAAACAGGTTCCAGCTGGTTTTCTACCTCTCCCTTAGTTCCACCAGA
                                                           GGAAAGAACCAAAGTTTGCAGAAGATACAGAAAACTCCTCTTTTGTGGCGGCGATCTGT
                                                                                 GlnLysSerArgCysLeuArgAsnLeuMetLysThrProLeuPheValValIleThrCys
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 125
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, M
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL000790
CURRENT APPLICATION NUMBER: US/09/949,002
CURRENT APPLICATION NUMBER: US/09/949,002
CURRENT FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: 60/231,401
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
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                                                                                        ; ORGANISM: Human US-09-949-002-656
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                                                                                                                                                                                                         Sequence 656, Application US/09949002

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, M
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL000790
CURRENT FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: 60/231,401
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
                                                                                                                          SEQ ID NO 656
LENGTH: 60194
TYPE: DNA
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                             uProGluGluValThrLysGlyAsnGlyTyrLeuGlnLysMetValSerIleSerAspIl
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 697
LENGTH: 66195
TYPE: DNA
ORGANISM: Human
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GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
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                                   ArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMetThrGluAspSerAlaGlnAla
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Sequence 6819, Application US/09724676
(GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative sp.
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
LENGTH: 3210
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                                                                                                                                                                                                              CCTGCCTTCCAAGAATTTCTTGCGGGGATGAGGCTGATTGAACTCCTGGATTCAGATAGG
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                                                                                 GTAAGCGCCTACAACAATTTTTTGAACTATGTCTCCAGCCTCCCTTCAACAAAAGCAGGG
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DB:
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GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
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LENGTH: 3210
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TYPE: DNA
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PheTyrAspLeuLeuIleGlnLysAsnLysHisLysHisLysGlyValAlaAlaSerAsp
                                                                                                GGAAAGAACCAAAGTTTGCAGAAGATACAGAAAACTCCTCTTTGGTGGCGGCGATCTGT
                                                                                                                              GlnLysSerArgCysLeuArgAsnLeuMetLysThrProLeuPheValValIleThrCys 345
                                                                                                                                                              ATATTACGGAAGCTCTTTTCACATAATATGACTCGTCTGCGAAAGTTTATGGTTTACTTT
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APPLICANT: Compugen LTD
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative
FILE REFERENCE: 129181.4 Compugen
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CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
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Sequence 6801, Application US/09724676A

GENERAL INFORMATION:
APPLICANT: Compugen LTD

TITLE OF INVENTION: Variants of alternative sp
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A

CURRENT FILING DATE: 2000-11-28

NUMBER OF SEQ ID NOS: 97222

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ATGTGCTTGATGAGCAAATTTACAGCCCAGAGACTAAGACCATTCTACCGGTTTTTAAGT
                                                                                                                                                                                                                                                                                                                                                GlnLysSerArgCysLeuArgAsnLeuMetLysThrProLeuPheValValIleThrCys
                  ThrGlyLeuLeuCysLysTyrThrAlaGlnArgPheLysProLysTyrLysPhePheHis
                                                                                 PheAspPheGluLeuGlnAspVal-----SerSerValAsnGluAspValLeuLeuThr
                                                                                                                                                                                                                                                                                                                             GAAAGAACCAAAGTTTGCAGAAGATACAGAAAACTCCTCTCTTTGGTGGCGGCGATCTGT 1676
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                                                                                                                             CTCAAAGCAACTGTGTCCTCCTGTGGTGAGCTGGCCTTGAAAGGGTTTTTTTCATGTTGC 1841
                                                                                                                                                PheIleArgSerLeuAspHisCysGlyAspLeuAlaLeuGluGlyValPheSerHisLys
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                                                                                                                                                                                                                                                             GCT---CATTGGTTTCAGTATCCTTTTGACCCATCCTTTGATGATGTG-----GCTGCT 1727
                                                                                                                                                                                                                                                                                             AlaIleGlnMetGlyGluSerGluPheHisSerHisThrGlnThrThrLeuPheHisThr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GATGACTACAAAGAAATATGTTCAATCCCT---CAAGTCATAGGAAAACTGATTCAAAAA 1436
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                                                              TTTGAGTTTAATGATGATGATCTCGCAGAAGCAGGGGTTGATGAAGATGAAGATCTAACC
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RESULT 15

US-09-724-676-6810

Sequence 6810, Application US/09724676

GENERAL INFORMATION:

APPLICANT: Compugen LTD

TITLE OF INVENTION: Variants of alternative sp.

FILE REFERENCE: 129181.4 Compugen

CURRENT APPLICATION NUMBER: US/09/724,676

CURRENT FILING DATE: 2000-11-28

NUMBER OF SEQ ID NOS: 97222

SOFTWARE: Patentin version 3.2

SOFTWARE: Patentin version 3.2

TYPE: DNA

ORGANISM: Homo sapiens
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CCTGCCTTCCAAGAATTTCTTGCGGGGATGAGGCTGATTGAACTCCTGGATTCAGATAGG
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ArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMetThrGluAspSerAlaGlnAla
                              AACCACTTATCCCGGACCTGCCTATTGATTGCTGTCCGTACAAACAGGGCCCAGGGACATC
                                                            AsnHisArgPheLysAsnMetValIleValThrThrThrThrGluCysLeuArgHisIle
                                                                                                                             AspGlyTyrAsnGluPheLysProGlnAsnCysProGluIleGluAlaLeuIleLysGlu
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                                                                                                                                                                                               CCCAAAATTGTGTCTCATTTG
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                                              GTAAGCGCCTACAACAATTTTTTGAACTATGTCTCCAGCCTCCCTTCAACAAAAGCAGGG
                                                                      ThrSerThrTyrSerSerLeuLeuArgTyrThrCysGly---SerSerValGluAlaThr
                                                                                                                                                CCTGCCTTCCAAGAATTTCTTGCGGGGATGAGGCTGATTGAACTCCTGGATTCAGATAGG
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Search completed: January 31, 2003, 11:50:02 Job time : 402 secs

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Command line parameters:

MODEL-frame+_p2n.model _DEV-xlh

-Q-cgn2_1/USPTO_spool_US9697089/runat_29012003_092753_19716/app_query.fasta_1.981

-Q-cgn2_1/USPTO_spool_US960189/runat_29012003_092753_19716/app_query.fasta_1.981

-Q-cgn2_1/USPTO_spool_US960189/runat_29012003_092753_19716/app_query.fasta_1.981

-Q-cgn2_1/USPTO_spool_US960189/runat_29012003_092753_19716/app_query.fasta_1.981

-Q-cgn2_1/USPTO_Spool_US960189/runat_29012003_092753_19716-NCDU-6-1CQAL

-Q-cgn2_1/USPTO_SPOOR_SCALE_1_1_3568_erunat_29012003_092753_19716-NCDU-6-1CQU-3

-NO_XLPXY_NO_MARA_-LARGEQUERY -NGC_SCORES-0-NAITY-LONGLOG-DEV_TIMEDUT-120

-NARN_TIMEDUT-30-THREADS-1_XGAPOP-10-XGAPEXT-0.5-FGAPOP-6-FGAPEXT-7

-WARN_TIMEDUT-30-THREADS-1_XGAPOP-10-XGAPEXT-0.5-FGAPOP-6-FGAPEXT-7
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Maximum Match 100%
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    nucleic search, using frame_plus_p2n model

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Ygapop 10.0 , x
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Delop 6.0 , C
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Card domain containing polypeptides, encoding nucleic acids,
                                                                                                                          Eukaryota; Metazoa;
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                                (bases 1 to 768)
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                                                       Reed,J.C., Pio,F.F., Godzik,A., Stehlik,C.,
Oliveira,V.A., Hayashi,H. and Pawlowski,K.
Card domain containing polypeptides, encoding
                            Patent: WO 0190156-A 98 29-NOV-2001;
                                            methods of use
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Location/Qualifiers
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QDLKDLYHTPSFLNFYPLGEDIDIIFNLKSTFTEPVLWRKDQHHHRVEQLTLVL"
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                     Submitted (21-FEB-2001) Program on Apoptosis Research, The Burnham Institute, 10901 North Jolla, CA 92037, USA
                                                                                                                Damiano, J.S., Stehlik, C., Pio, F., Go
Clan, a novel human ced-4-like gene
Genomics 75 (1-3), 77-83 (2001)
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Stehlik,C., Damiano,J.S., Pio,F.,
                                                          Direct Submission
                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
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KVEQDAARGIIHMILKKGSESCNLFLKSLKEWNYPLFQDLNGQSGLTDSLGNLKNLTK
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ARLVGWQFDDDDLSVITGAFKLVTA"
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LMLPWGCDVQGSLSSLLKHLEEVPQLVKLGLKNWRLTDTEIRILGAFFGKNPLKNFQQ
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Biochem. Biophys. Res. Commun.
                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleoston Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 313) Geddes, B.J., Wang, L., Huang, W.-J., Lavellee, M., Manji, G.A., Brown, M., Jurman, M., Morganstern, J., Merriam, S., Glucksmann, A., Distefano, P.S. and Bertin, J.

Distefano, P.S. and Bertin, J.
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//Protein_id="AAK14777.1"
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LMLPWGCDVQGSLSSLLKHLEEVPQLVKLGLKNWRLTDTEIRILGAFFGKNPLKNFQQ
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277. .1356
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1. .1395
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/db_xref="taxon:9606"
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                    PheGlnAspLeuAsnGlyGlnSer
                                                                                                                                                                                                                                                                 AGCAAATCACAGATGACCTATTTGTATGGAATGTTCTGAATCGCGAAGAAGTAAACATC
                                                                                                                                                                                                                                                                                        LysGlnIleThrAspAspLeuPheValTrpAsnValLeuAsnArgGluGluValAsnIle 40
                                                                                                               LysGlySerGluSerCysAsnLeuPheLeuLysSerLeuLysGluTrpAsnTyrProLeu 80
                                                                                                                                                                           ATTTGCTGCGAGAAGGTGGAGCAGGATGCTGCTAGAGGGATCATTCACATGATTTTGAAA
                                                                                                                                                                                                                                                                                                                                                      ATGAATTTCATAAAGGACAATAGCCGAGCCCTTATTCAAAGAATGGGAATGACTGTTATA
                                                                                        AAGGGTTCAGAGTCCTGTAACCTCTTTCTTAAATCCCTTAAGGAGTGGAACTATCCTCTA
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Kveqdaargiihiilkkoseschielksikemayplfodlagglfhotseolldla
Odlkdivftpseplinfylegedtdiirirklkstfeplfhogskrohhrregutlikglag
LQSPCIIEGESGKKSTLLQRIAMLWGSGKCKALTKFKFVFFLRLSRAQGGLFETLCD
OLLDIPGTIRKOTFMAMLLKLRORVLFLLDGYNEFKPONCPEIEALIKRENHFKNMVI
VTTTTECLRHIROFGALTAEVGDMTEDSAQALIREVLIKELAEGLLLQIQKSRCLRNL
NKTPLFVVITCALQMGESEFHSHTQTTLFHTFVDLLIQKNKHKHKGVAASDFIRSLDH
KTPLFVVITCALQMGESEFHSHTQTTLFHTFVDLLIQKNKHKHKGVASDFIRSLDH
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LAAVYQHGCLLGISIAKRFURFQESLGSVKNTTEQETLKAININSFVECGIHLYQEST
SKSALSQEFERFFOGKSLYINSGNIDDYLFDFFEHLENCASALDFIKLDFYGGAMASH
RESULTSHEFERFOGKSLYINSGNIDDYLFDFFEHLENCASALDFIKLDFYGGAMASH
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IFSSATSLRLQIKRCAGVAGSLSLVLSTCKNIYSLMVEASPLTIEDERHITSVTNLKT
LSIHDLQNQRLPGGLTDSLGNLKNLTKLIMDNIKMNEEDAIKLAEGLKNLKKMCLFHL
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/note="LRR;
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KNWRLTDTEIRILGAFFGKNPLKNFQQLNLAGNRVSSDGWLAFWGVFENLKQLVFFDF
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US-09-697-089-2_COPY_1_88 (1-88) x AY035391 (1-3219)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Poyet, J.-L., Alnemri, E.S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens ICE-protease activating face AY035391
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VTTTECLERHIRQFGALTAEVGDMTEDSAQALIREVLIKELAEGLLLQIQKSRCLRNL
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SKSALSGEFBAFFGKKSLYINSGNIFDYLFDFFEHLPNCASALDFIKLDFYGGAMASP
SKSALSGEFBAFFGKKSLYINSGNIFDYLTDFFEHLPNCASALDFIKLDFYGGAMSP
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FSSATSGLFALDIKTGAVAGSISLVLSTCKNIYSLMYEASPLTIEDERHITSVTNLKT
                                                                                                                                                                                                                                                                                        KNWRLTDTEIRILGAFFGKNPLKNFQQLNLAGNRVSSDGWLAFMGVFENLKQLVFFDF
STKEFLPDPALVRKLSQVLSKLTFLQEARLVGWQFDDDDLSVITGAFKLVTA"
                                                                                                                                                                                                                                                                                                                                     THLSDIGEGMDYIVKSLSSEPCDLEEIQLVSCCLSANAVKILAQNLHNLVKLSILDLS
ENYLEKDGNEALHELIDRMNVLEQLTALMLPWGCDVQGSLSSLLKHLEEVPQLVKLGL
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/db_xxef="GI:14334215"
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KVEQDAARGIIHMILKKGSESCNLFLKSLKEWNYPLFQDLNGQSLFHQTSEGDLDDLA
                                                                                                                                                                                                                                                                                                                                                                                     LSIHDLQNQRLPGGLTDSLGNLKNLTKLIMDNIKMNEEDAIKLAEGLKNLKKMCLFHL
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LQSPCIIEGESGKGKSTLLQRIAMLWGSGKCKALTKFKFVFFLRLSRAQGGLFETLCD
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/protein_id="AAK59843.1"
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recruitment domain containing protein"
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1 MetAsnPheILeLysAspAsnSerArgAlaLeuIleGlnArgMetGlyMetThrValIle

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TITLE
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                                                                                                                                                                                                                                                                                                                                               Submitted (04-JUL-2002) Takao Isogai, FLJ Project(HRI Team); 2-6-7 Submitted (04-JUL-2002) Takao Isogai, FLJ Project(HRI Team); 2-6-7 (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) NEDO human cDNA sequencing project supported by Ministry of Reonomy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ninomiya,K., Wagatsuma,M., Kanda,K., Kondo,H., Yokoi,T., Kodaira,H., Furuya,T., Takahashi,M., Kilkawa,E., Omura,Y., Ak Kandhara,K., Katsuta,N., Sato,K., Tanikawa,M., Yamazaki,M., Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Wakamatsu,A., Ishiyamamoto,J., Isono,Y., Kawai-HiO,Y., Saito,K., Nishikawa,T., Kimura,K., Yamashita,H., Matsuo,K., Nakamura,Y., Sekine,M., Kikuchi,H., Murakawa,K., Kanehori,K., Takahashi-Fujii,A., Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S., Nagahari,K., Masuho,Y., Nagai,K. and Isogai,T. NEDO human cDNA sequencing project upublished
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Isogai,T. and Yamamoto,J.
Direct Submission
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Mammalia; Eutheria; Primates;
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                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="D9OST2003791"
/cell_type="CD34+ Cells"
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                                                                                                                                                                          /note="cloning vector: pME18SFL3~mRNA from CD34+ cells
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                                                                                                                                                                          Clone distribution: MCC clone distribution information can be for through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 50 Row: a Column: 10 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genom
                                                                                                                                                                                                                                                                                                      Gunaratne, P.H., Garcia, A.M., Lu, Yoon, V.S., Kowis, C.R., Lawrence, Richards, S., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                    Sequencing Center
Center code: BCM-HGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (06-JUN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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Mammalia; Eutheria; Primates;
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MGC:35330 IMA
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Contact: amg@bcm.tmc.edu
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/organisme"Homo sapiens"
/db_xref="LocusID:58484"
/db_xref="taxon:9606"
/clome="MGC:35330 IMAGE:5179909"
/tissue_type="Brain, Lung, Testis
                                                                                                                                  Location/Qualifiers
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      Testis,
                                                                                                                                                                                                                                                                                                                               Hulyk, S.W., Hale, S.M. Martin, R.G., Muzny, D.
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                                                                                                                                                                                                                                                                                           ATTTGCTGCGAGAAGGTGGAGCAGGATGCTGCTAGAGGGATCATTCACATGATTTTGAAA
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Sequence
AX318091
Reed, J.C., Pio, F.F., Godzik, A., Stehlik, C., Oliveira, V.A., Hayashi, H. and Pawlowski, K.
                                                Homo sapiens
Eukaryota; M
                                      Mammalia; Eutheria;
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KVEQDAARGIIHMILKKGSESCNLFLKSLKEWNYPLFQDLNGQSLFHQTSEGDLDDLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="caspase recruitment domain
/protein_id="AAH31555.1"
/db_xref="GI:21594976"
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/lab_host="DH10B"
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                                              3396 bp
Homo sapiens CLANA (CLANI) mRNA,
AY027787
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Homo sapiens
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Patent: WO 0190156-A 96 29-NOV-2001;
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RGDLALEGVFSHKFDFELQDVSSVNEDVILTTGLLCKKTÄQRFKFKYKFFKKSFQEYT
AGRELSSLLTSHEPEBYFKGNOYLOKAVSIBDITSTYSSLLRYTGGSSVEATRAVNKH
LAAVYOHGCLLGLSIAKRPLRRQESLOSVKNTTEQEIIKAININSFYBCGIHLYOEST
SKSALSDEFEAFFQKSIYINSONIPDYLFDFFFHLENCASALDFIKLDFYGGAMASW
EKAAEDTGGIHMEAPETYIBSRAVSLFFNWKOEFRTLEVTLRDFSKLNKDIRYLKF
EKSALSGEIHMEAPETYIBSRAVSLFFNWKOEFRTLEVTLRDFSKLNKDIRYLKF
LSIHDLONGRLFGGLTDSLGNLKNLTKLINDNIKTMEABDLKILAGLKNLKKLEFHL
THLSDIGEGMDYIVKSLSEPODLEETQLVSCCLSANAVKILAQNLHHLYKLSILDLS
ENYLEKDGNEALHELIDRMNVLEDLTALMLFWGCDVGSLSSLKHHEEVPOLVKLGI
ENYLEKDGNEALHELIDRMNVLEDLTALMLFWGCDVGSLSSLKHHEEVPOLVKLGI
ENYLEKDGNEALHELIDRMNVLEDLTALMLFWGCDVGSLSSLKHHEEVPOLVKLGI
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STKEFLPDPALVRKLSQVLSKLTFLQEARLVGWQFDDDDLSVITGAFKLVTA"
1 737 c 793 g 874 t
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/db_xref="taxon:9606"
277. .3351
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VTTTTECLRHIRQFGALTAEVGDMTEDSAQALIREVLIKELAEGLLLQIQKSRCLRNL
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LQSPCIIEGESGKGKSTLLQRIAMLWGSGKCKALTKFKFVFFLRLSRAQGGLFETLCD
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                      IleCysCysGluLysValGluGlnAspAlaAlaArgGlyIleIleHisMetIleLeuLys 60
                                                                                                                                                                                          ATGAATTTCATAAAGGACAATAGCCGAGCCCTTATTCAAAGAATGGGAATGACTGTTATA 336
                                                                                             AAGCAAATCACAGATGACCTATTTGTATGGAATGTTCTGAATCGCGAAGAAGTAAACATC
ATTTGCTGCGAGAAGGTGGAGCAGGATGCTAGAGGGATCATTCACATGATTTTGAAA
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Damiano,J.S., Stehlik,C., Pio,F., Go
Clan, a novel human ced-4-like gene
Genomics 75 (1-3), 77-83 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Stehlik,C., Damiano,J.S., Pio,F., Godzik,A. and Direct Submission
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SKSALSQEFEAFFGGKSLYINGGNIDVLFDFFEHLENGASALDFIKLDFYGGAMASW
EXAARDTGGIHMEBAPETYIPSANSVSLFFNNKQEFRTLEVTLRDFSKLMKDIRYLGK
IFSSATSLRLOIKRCAGVAGSLSLVLSTCKNIYSLMVEASPLTIEDERHITSVTNLKT
ISIHDLQNQRLPGGLTDSLGNLKNLTKLIMDNIKMNEEDAIKLÆGLKNLKKKCLFHL
THLSDIGEGMYDIVKSLSEPCDLEEEIQLVSCCLSANAVKILAQNLHNLKKLSILDLS
ENYLEKDGGNEALHELIDRMNVLEQLTALMLPWGCDYQGSLSSLLKHLEEVPQLVKLGL
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QLDJTGTIRKQTFMAMLLKLAQRVLFFLLDGYNEFKPQNCPEIEALIKENHRFKNMVI
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MKTPLTVITCAIQMCBALTAEVGDMTEDSAQAIL REVLIKEHLEGLLQLIKSRCLRH
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AGRRLSSLLTSHEPEEVTKGNGYLQKNVSISDITSTYSSLLRYTCGSSVEATRAVMKH
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277. .3351
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737 c 793 g 874 t
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Gingras, M.-C., Qiu, J
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Gingras,M.-C., Qiu,J. and Margolin,J.F.
Differential expression of the caspase recruitment domain protein
12 (CARD12) during monocytic differentiation
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/protein_id="AAK53443.1"
/db_xref="Gi:14040075"
/translation="MNFIKDNSRALIORMGMTVIKQITDDLFVWNVLNREEVNJICCE
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Card domain containing polypeptides, encoding nucleic acids, and
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                                                                             LysGlnIleThrAspAspLeuPheValTrpAsnValLeuAsnArgGluGluValAsnIle 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (18-APR-2002) Genoscope - GBP 191 91006 EVRY cedex - FRANCE (E-GBP 1910-006 EVRY cedex - FRANCE) (E-WW-genoscope.cns.fr)
On Mar 6, 2000 this sequence version
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Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 138909)
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GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd

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Command line parameters:

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-O-MODEL-frame+_p2n.model -DEV=xlh
-O-MODEL-frame+_p2n.model -DEV=xlh
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-DB-N_Geneseq_101002 -OFMT-fastap -SUFFIX-p2n.mg -MINMATCH-0.1 -LOOPCL-0
-LOOPEXT-0 -UNITS-bits -START-1 -END--1 -MATRIX-blosum62 -TRANS-human40.cdi
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-WARN_TIMEOUT-30 -THREADS-1 -XGAPOP-10 -XGAPEXT-0.5 -FGAPOD-6 -FGAPEXT-7
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SUMMARIES

| 4 | 44 | 43 | 42 | 41 | 40 | 39 | 38 | 37 | 36 | 35 | 34 | 33 | 32 | 31 | 30 | 29 | 28 | 27 | 26 | 25 | 24 | 23 | 22 | 21 | 20 | 19 | 18 | 17 | 16 | 15 | 14 | 13 | 12 | 11 | 10 | و | œ | 7 | თ | տ | 4 | 3 | 2 | 1 | Result No. |
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| 9 | 95 | 95 | 95 | 95 | 95 | 96.5 | 96.5 | 96.5 | 96.5 | 96.5 | 96.5 | 97 | 97 | 97 | 97 | 97 | 97 | 100 | 100 | 102 | 102 | 102.5 | 103.5 | 103.5 | 108 | 108 | 108 | 108 | 108 | 108 | 118.5 | 118.5 | 118.5 | 118.5 | 392 | 5 | S | 458 | 461 | | 461 | 461 | 461 | | Score |
| 20.6 | 20.6 | 20.6 | 20.6 | 20.6 | 20.6 | 20.9 | 20.9 | 20.9 | 20.9 | • | • | • | | | • | 21.0 | 21.0 | 21.7 | 21.7 | 22.1 | 22.1 | 22.2 | • | • | 23.4 | 23.4 | 23.4 | 23.4 | • | 23.4 | 25.7 | 25.7 | 25.7 | | 85.0 | 99.1 | 99.1 | • | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 0 | Query Match |
| 1216 | 1216 | 1215 | 1215 | 1215 | 1215 | 2669 | 2662 | 2662 | 1252 | 879 | 549 | 5059 | 4556 | 4466 | 3863 | 1487 | 1183 | 3151 | 2862 | 2580 | 2580 | 321 | 1215 | 429 | 3732 | 3532 | 3532 | 3532 | 2589 | 1435 | 1560 | 1560 | 1215 | 1215 | 2215 | 3615 | 261 | 3213 | 3545 | ũ | 3133 | | 9 | σı | Length |
| 2.2 | 20 | 24 | 22 | 20 | 17 | 22 | 22 | 22 | 24 | 23 | 24 | 22 | 22 | 22 | 22 | 22 | 22 | 19 | 18 | 24 | 18 | 24 | 22 | 22 | 19 | 24 | 20 | 18 | 18 | 17 | 21 | 20 | 21 | 20 | 22 | 22 | 24 | 22 | 22 | 24 | 22 | 24 | 24 | 24 | DB |
| AAF90184 | AAX01277 | ABT03964 | AAF24471 | AAX81217 | AAT03179 | AAK86923 | AAK86925 | AAK86924 | ABK14805 | AAS75669 | ABK12898 | AAF83652 | AAD02764 | AAD02765 | AAS34888 | AAD02763 | AAS35011 | AAV55043 | AAT61592 | ABK93871 | AAT70838 | ABK22730 | AAI66509 | ABA09527 | AAV55040 | ABN96857 | AAZ22143 | AAT72711 | AAT61590 | AAT43709 | AAA13796 | AAX27727 | AAA13794 | AAX27725 | AAH78218 | AAS03946 | ABK22765 | AAH78219 | AAH98254 | ABK22731 | AAS03945 | ABK22732 | ABK22734 | ABK22733 | ID |
| Human interleukin- | Human ICE coding s | | Human pre-interleu | Nucleotide sequenc | \vdash | Human immune/haema | | ` | | _ | | CARD-8 pc | NAC | Human NAC gamma or | cDNA encoding nove | Human CARD contain | q | Murine HIAP-2 codi | Murine c-IAP. Mus | | Human apoptosis in | _ | Pig caspase coding | _ | Human HIAP-2 codin | Gene #3355 used to | Human cellular inh | inhibitor | | ₽- | | | | Canine interleukin | | casp | | Nucleotide sequenc | e EST | | caspa | CDNA | | man cD | Description |

ALIGNMENTS

RESULT 1 ABK22733; ABK22733 standard; cDNA; 578 ВP

26-MAR-2002

(first

entry)

inflammatory hyperplasia; fibrosis; smooth muscle cell proliferation; balloon angioplasty; restenosis; glioma; carcinoma; sarcoma; melanoma leukaemia; allergy; arthritis; lupus; Schrogen's syndrome; Crohn's disease; graft-versus-host disease; stroke; myocardial infarction; heart failure; neurodegenerative disease; Caspase recruitment domain; CARD; ss; NB-ARC; ANGIO-R; LRR; SAM; abnormal cell proliferation; cancer; abnormal cell death; apoptosis; autoimmune disease; inflammation; keratinocyte hyperplasia; Human cDNA encoding CLAN C. melanoma;

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                                                                                                                                                                                                                                                                                                                                                  containing the vector (e.g. bacteria, yeast, plant, animal, mammalian CC and insect cells) and an anti-CARD antibody. The CARD-containing polypeptide and CARD-encoding nucleic acid are useful for treating a pathology characterised by abnormal cell proliferation (e.g. cancer), antoinmune diseases or inflammation. In particular, the polypeptide and nucleic acid are useful for treating a comparity of the polypeptide and nucleic acid are useful for treating a comparity of the polypeptide and nucleic acid are useful for treating content of the polypeptide and nucleic acid are useful for treating content of the polypeptide and nucleic acid are useful for treating content of the polypeptide and nucleic acids are useful for treating content of the polypeptide and nucleic acids, smooth content of the polypeptide and nucleic acids are useful content of the polypeptide and nucleic acids are useful content of the polypeptide and nucleic acids are useful content of the polypeptide and nucleic acids are useful content of the polypeptide and containing protein.
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wlowski K;
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                  The invention relates to an isolated caspase recruitment domain (CARD) containing polypeptide, or a CARD, NB-ARC, ANGIO-R, IRR or SAM domain from it, and the polynucleotides encoding them. Also included are a recombinant vector comprising the polynucleotide, recombinant cells containing the vector (e.g. bacteria, yeast, plant, animal, mammalian and insect cells) and an anti-CARD antibody. The CARD-containing polypeptide and CARD-encoding nucleic acid are useful for treating a pathology characterised by abnormal cell proliferation (e.g. cancer), abnormal cell death (apoptosis), autoimmune diseases or inflammation. I particular, the polypeptide and nucleic acid are useful for treating keratinocyte hyperplasia, inflammatory hyperplasia, fibrosis, smooth muscle cell proliferation in arteries following balloon angioplasty
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New caspase recruitment domain (CARD)-containing polypeptides and encoding nucleic acids, useful for treating abnormal cell proliferation or cell death, autoimmune diseases or inflammation, e.g. carcinomas,
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10-OCT-2000; 2000US-0686347.
14-MAR-2001; 2001US-275980P.
23-MAY-2001; 2001US-0864921.
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14-MAR-2001;
23-MAY-2001;
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                                                                                                                                                                                                                                              Caspase recruitment domain; CARD; ss; NB-ARC; ANGIO-R; LR; abnormal cell proliferation; cancer; abnormal cell death;
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                                                          24-MAY-2001;
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Best Local Similarity:
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Pawlowski K;
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Score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isolated caspase recruitment domain-12 polypeptide and nucleic acids encoding them, useful for treating and diagnosing disorders associated with abnormal apoptosis such as cancer, arthritis and Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Caspase recruitment domain; CARD-12; apoptosis; stress-related pathway; cancer; viral infection; poxvirus; adenovirus; autoimmune disorder;
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                                                                                                                                                                                                                                                                                                                       Crohn's disease, insulin-dependent diabetes, contact dermatitis, psoriasis, graft rejection), bacterial infections (e.g. tuberculosis, lepromatous leprosy), ischaemic and hypoxic brain injury, kidney
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meningitis and liver or
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10-OCT-2000;
14-MAR-2001;
23-MAY-2001;
                                                                                                                                                                                                                                                                                                                                          Caspase recruitment domain; CARD; ss; NB-ARC; ANGIO-R; LRR; SAM; abnormal cell proliferation; cancer; abnormal cell death; apoptosis; autoimmune disease; inflammation; keratinocyte hyperplasia; inflammatory hyperplasia; fibrosis; smooth muscle cell proliferation; balloon angioplasty; restenosis; glioma; carcinoma; sarcoma; melanoma leukaemia; allergy; arthritis; lugioscrafta; syndrome; Crohn's disease; graff-versus-host disease; stroke; myocardial infarction; heart failure; neurodeenerative disease;
                                       New caspase recruitment de
encoding nucleic acids, us
or cell death, autoimmune
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73)
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; 2000US-0686347.
; 2001US-275980P.
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                                                                                                                     Hayashi
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                                       domain (CARD)-containing polypeptides and useful for treating abnormal cell proliferatine diseases or inflammation, e.g. carchomas,
                                                                                                                      Pawlowski
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                                                                                                                     Stehlik C,
wlowski K;
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Page 166-171;

216pp; English

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RESULT 6
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AC AAH1
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                                 WO200154477-A2
                                                                   Mus musculus
                                                                                                   biodiversity;
                                                                                                                    diagnostics; forensic test;
                                                                                                                                    Human; sheep; p:
tomato; monkey;
                                                                                                                                                                                        Murine
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                                                                                                                                                                                                                                                         AAH98254;
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                                                                                                                               cow; fruit fly; yeast; hamster; macaque; g; sea urchin; expressed sequence tag; ES
                                                                                                   therapy;
                                                                                                                                                                                    coding sequence SEQ ID NO: 111.
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                                                                                                   gene mapping; genetic disorder;
nutrition; ss.
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17-JUL-2000;
03-AUG-2000;
15-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention provides the protein and coding sequences of novel proteins from a variety of organisms, including human, dog, cat, horse, cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea urchin and tomato. These were derived from expressed sequence tags (ESTs from the organism of interest. They can be used in diagnostics, forensics, gene mapping, identification of mutations, to assess biodiversity and for nutritional purposes. The present sequence is a cDN processity and for nutritional purposes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolated polypeptide for treatment antibodies and research use -
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P-PSDB; AAM23595.
                  Nucleotide sequence of a human secreted polypeptide
                                        26-NOV-2001
                                                             AAH78219;
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Drmanac RA,
                                                                                  standard;
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2000US-0617746.
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2000US-0663870.
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Human; secreted polypeptide; nervous disease; muscular disease; tumour;

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                                             US-09-697-089-2_COPY_1_88 (1-88) x
                                                                                                                                                                    Alignment
                                                                                                                                                                                                                                      The present sequence encodes a human secreted polypeptide. The secreted polypeptides and polynucleotides are useful for treating recreated polypeptides and polynucleotides are useful for treating nervous and muscular diseases, for inhibiting tumour formation and metastasis, for treating gastrointestinal ulceration, for preventing and treating diseases in spinal cord, thyroid gland, ovary, prostate, renal gland, small intestine, heart, trachea, thymus, lymph node, muscular system and colon, for treating lipase deficiency in cystic fibrosis and pancreatitis, for treating undesirable clot formation such as myocardial infarction, during angioplasty and all surgical procedures that require decreased blood clot formation, for treating limune disorders, for treating inflammation and transplant rejection, for enhancing bone thickness and increasing bone density, for reducing the loss of essential ferroxidases, for suppressing apoptosis, and for regulating vascular smooth cell proliferation. They
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13-MAR-2000;
03-OCT-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel isolated secreted polypeptide useful for treating nervous and muscular diseases, gastrointestinal ulceration, coagulation and immudisorders, microbial diseases, inflammation and transplant rejection
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)B; AAG67527.
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2000US-0188916.
2000US-0236874.
2000US-0237846.
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                                                                                                                                                                                                                                                                                           24-MAY-2000;
10-OCT-2000;
14-MAR-2001;
23-MAY-2001;
The invention relates to an isolated caspase recruitment domain (CAR -containing polypeptide, or a CARD, NB-ARC, ANGIO-R, LRR or SAM doma from it, and the polynucleotides encoding them. Also included are a recombinant vector comprising the polynucleotide, recombinant cells containing the vector (e.g. bacteria, yeast, plant, animal, mammalia and insect cells) and an anti-CARD antibody. The CARD-containing
                                                                                                                                                                                                                           Reed JC,
Oliveira
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                                                                                                                                 New caspase recruitment domain (CARD)-containing polypeptides and encoding nucleic acids, useful for treating abnormal cell proliferation or cell death, autoimmune diseases or inflammation, e.g. carcinomas,
                                                                                                                                                                                                                                                                                                                                                           24-MAY-2001;
                                                                                            Claim
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                                                                                                                 Homo
                                                                                                                                                                    excitotoxic
                                                                                                                                                                                                                 aplastic anaemia; myocardial infarction; inflammatory disorder; Crohn's disease; insulin-dependent diabetes; contact dermatitis; psoriasis; graft rejection; bacterial infection; lepromatous leptuberculosis; ischaemic brain injury; hypoxic brain injury; ds;
                                                                                                                                                                                                                                                                                                                             systemic lupus erythematosis; arthritis; neurological disorder; stroke; Alzheimer's disease; amytrophic lateral sclerosis; haematologic diseas
                                                                                                                                                                                                                                                                                                                                                                                   cancer; viral infection; poxvirus; adenovirus; autoimmune disorder;
                                                                                                                                                                                                                                                                                                                                                                                                            Caspase recruitment domain; CARD-12; apoptosis; stress-related pathway;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human caspase recruitment domain 12 (CARD-12) genomic DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       standard;
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                                                                                                                                                                 haemic brain injury; hypoxic brain injury; ds; reperfusion injury; acute bacterial meningitis; damage; liver disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                   CC The sequence represents a genomic DNA which encodes the human caspase CC recruitment domain 12 (CARD-12) polypeptide. CARD domains are found in a CC number of proteins that transmit signals that activate apoptosis and CC inflammatory pathways in response to stress and other stimuli. Therefore, CC CARD-12 and its corresponding nucleic acid may be used in treatment and CC diagnosis of patients suffering from disorders associated with an CC abnormal level (an increase or a decrease) of apoptotic cell death or CC abnormal activity of stress-related pathways. The disorders include CC cancer, viral infections (e.g. caused by poxviruses, adenoviruses), CC autoimmune disorders (e.g. systemic lupus erythematosis, arthritis), CC neurological disorders (e.g. Alzheimer's disease, amyotrophic lateral CC sclerosis), haematologic diseases (e.g. aplastic anaemia, myocardial CC infarction, stroke), inflammatory and immune system disorders (e.g. CC crohn's disease, insulin-dependent diabetes, contact dermatitis, CC psoriasis, graft rejection), bacterial infections (e.g. tuberculosis, contact dermatitis, CC ischaemia/reperfusion injury, schiemic brain damage, acute bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   encoding them, useful fowith abnormal apoptosis
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RESULT
AAH7821
The present sequence encodes a human secreted polypeptide. The conservation of the present sequence encodes and polypucleotides are useful for treating concervous and muscular diseases, for inhibiting tumour formation and metastasis, for treating gastrointestinal ulceration, for preventing and treating diseases in spinal cord, thyroid gland, owary, prostate, cand treating diseases in spinal cord, thyroid gland, owary, prostate, consucular system and colon, for treating lipase deficiency in cystic fibrosis and pancreatitis, for treating undesirable clot formation could be a myocardial infarction, during angioplasty and all surgical concedures that require decreased blood clot formation, for treating treating immune disorders, for treating inflammation and transplant concedures that require decreased blood clot formation, for treating treating immune disorders, for treating inflammation and transplant conceduring the loss of essential ferroxidases, for suppressing the loss of essential ferroxidases.
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13-MAR-2000;
03-OCT-2000;
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                                                                                                                                                                                                                                                                                                                                        Novel isolated secreted polypeptide useful for treating nervous and muscular diseases, gastrointestinal ulceration, coagulation and immundisorders, microbial diseases, inflammation and transplant rejection
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        The invention relates to a canine interleukin 18 (dIL18) and a canine interleukin 1 beta convertase (dICE) which can cleave precursor forms of dIL18 and interleukin 1 beta to give the active forms. Host cells transformed by vectors comprising the dIL18 DNA (optionally with DNA coding for dICE) are used for the recombinant expression of the protein. The canine interleukin 18 is able to act on canine leukocytes to induce a factor potentiating the expression of class II MHC on canine tumour
                                                                                                                       Canine interleukin 18 and canine interleukin 1-beta convertase For treatment of immune disorders of dogs including cancer, allergies and inflammatory diseases.
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tumour cell; lymphocyte; Fas ligand; allergy;
infectious disease; skin inflammation; ss.
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11-DEC-1997;
06-JUL-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 dog; and to activate canine leukocytes to inhibit allergies. dII18 in combination with dII12 can be used for the treatment of immune disorders of dogs, such as cancer, allergies, infectious diseases or skin inflammation. The present sequence represents the coding sequence of
                    (TORA ) TORAY IND INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     No.:
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                                                                                                                                                                                                                                  dog;
                                                                                                                                                                                                                     disease; tumour;
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                                                                                                                                                                                                                                  interleukin 18;
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                                         97JP-0213754.
97JP-0341741.
98JP-0190594.
                                                                                    98JP-0220074
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RESULT 13
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes canine interleukin 18 (IL-18). Canine IL-18 is capable of inducing an antiviral activity factor and a factor reinforcing the expression of class II MHC molecules on canine tumour calls by reacting with canine leukocytes, promoting the growth of canine lymphocytes, reinforcing the expression of Fas ligand on canine lymphocytes and canine tumour cells, obstructing and killing canine tumour cells, reducing the tumour formed in a canine body and preventing canine allergy by activating canine leukocytes. Canine IL-18 is used for the treatment of canine inmune diseases. The present invention also describes the canine inmune diseases. The present invention also describes the canine incerleukin lbeta conversion enzyme (ICE), which has the ability of cleaving the precursor proteins of interleukin lbeta and IL-18 to convert them to their active types. The present sequence
                                                                                                                                                                         Canine interleukin-1 beta convertase encoding
                                                                                      Canis
                                                                                                                               Canine; interleukin 18; dIL18; interleukin 1 beta convertase; leukocyte; MHC; tumour cell; lymphocyte; Fas ligand; allergy;
                                                                                                                                                                                                         02-JUN-1999
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                                                                                                                 disorder; infectious disease;
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                                                                                                                                                                                                                                                                  standard;
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07-AUG-1998; 18-FEB-1999

98WO-JP03524.

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RESULT 14
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Query Match:
DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 coding for dICE) are used for the recombinant expression of the protein. The camine interleukin 18 is able to act on canine leukocytes to induce a factor potentiating the expression of class II MHC on canine tumour cells; to promote the proliferation of canine lymphocytes; to potentiate the expression of Fas ligand on canine lymphocytes and tumour cells; to damage and kill canine tumour cells; to reduce tumour size in the living dog; and to activate canine leukocytes to inhibit allergies. dII18 in combination with dII12 can be used for the treatment of immune disorders of dogs, such as cancer, allergies, infectious diseases or skin
             Canine interleukin lbeta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a canine interleukin 18 (dIL18) and a canine interleukin 1 beta convertase (dICE) which can cleave precursor forms dIL18 and interleukin 1 beta to give the active forms. Host cells transformed by vectors comprising the dIL18 DNA (optionally with DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Canine interleukin 18 and canine interleukin 1-beta convertase For treatment of immune disorders of dogs including cancer,
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                                         27-JUL-2000
                                                                        AAA13796
                                                                                                   AAA13796 standard; cDNA; 1560
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Conservative:
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11-DEC-1997;
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ICE; immune
                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                              CCAAATGCATGCCAGATTTTTATTTCTAATATTTTGCAATGAGGACATTCACCTGGCACAG
                                                     SerGluSerCysAsnLeuPheLeuLysSerLeuLysGluTrpAsnTyrProLeuPheGln
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disease; tumour;
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97JP-0341741.
98JP-0190594.
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                                                                         US-09-697-089-2_COPY_1_88 (1-88) x AAT43709 (1-1435)
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                                                                                                                                                                                                            Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                       A cDNA clone (AAT43709) codes for human inhibitor of apoptosis 1 (hIAP-1) (AAW04583), a protein useful for treating degenerative diseases, as an antiviral defence mechanism and for preventing cell death during stokes of trauma. The cDNA can be isolated from human Jurkat cell lines or human osteoclastoma stromal cell lines and incorporated into bacterial, mammalian or baculovirus expression vectors for use in prodn. of recombinant hIAP-1. It can also be utilised in the diagnosis or gene therapy of diseases related to hIAP-1 under-expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Polynucleotide encoding human inhibitor of apoptosis gene 1 - useful for treating degenerative diseases, as antiviral defence mechanism and preventing cell death during trauma and strokes
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Search completed: January 31, 2003, 13:24:16 Job time: 106.246 secs

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Command line parameters:

-MODEL-frame+_p2n.model -DEV-xlh
-O_-cgn2_1/USPTO_spool_VS9697089/runat_29012003_092754_19729/app_query.fasta_1.981
-O_-cgn2_1/USPTO_spool_VS9697089/runat_29012003_092754_19729/app_query.fasta_1.981
-OB-EST -OFMT-fastap -SUFFIX-p2n.rst -MINMATCH-0.1 -LOOPCL-0 -LOOPEXT-0
-UNITS-blts -STAKT-1 -END--1 -MATRIX-blosum62 -TRANS-human40.cd1 -LIST-45
-DOCALIGN-200 -THR_SCORE-pot -THR_MAX-100 -THR_MIN-0 -ALICN-15 -MODE-LOCAL
-OUTFMT-pto -NORM-ext -HEAPSIZE-500 -MINLEN-0 -MAXLEN-200000000
-USER-0S09697089_6CGN_1_1_1985_6runat_29012003_092754_19729 -NCPU-6 -TCPU-3
-NO_XLPXY -NO_MARP -LARGEQUERY -NG_SCORES-0 -NAIT -LONGLOG -DEV_TIMEOUT-120
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ALIGNMENTS

KEYWORDS SOURCE ORGANISM ACCESSION VERSION RESULT 1 BI908869 LOCUS DEFINITION EST

BI908869 603066455F1 NIH_MGC_118 Homo sapiens BI908869.1 GI:16171950 BI908869 mRNA sequence. Homo bp mRNA linear EST 16-OCT-2001 sapiens cDNA clone IMAGE:5215669 5',

REFERENCE AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleoston Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)

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Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11541 row: m column: 14
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High quality sequence stop: 744.
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Tissue Procurement: Life Technologies,
Homo sapiens
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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/db_xref="taxon:9606"
/clone="IMAGE:5215669"
/clone_lib="NIH_MGC_118"
/tissue_type="leukocyte"
/lab_host="DH10B"
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AQ889169
404 bp DNA linear GSS 10-NOV-1999 HS_2161_B1_A01_T7C CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2161 Col=1 Row=B, DNA sequence.
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Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies,
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
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/db_xref="taxon:9606"
/clone="IMAGE:5179909"
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Location/Qualifiers
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Seg primer: T7
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Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
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1 (bases 1 to 404)
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Tel: (206) 616-3618
Fax: (206) 616-3887
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Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S.,
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E-Col1 DH10B"
1 93 c 70 g 122 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="plate=2161 Col=1 Row=B"
/clone_lib="CIT Approved Human Genomic
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                                                                                                                                                                                                                                                                                                  LysGlnIleThrAspAspLeuPheValTrpAsnValLeuAsnArgGluGluValAsnIle 40
                                                                                                                  PheGlnAspLeuAsnGlyGln 87
                                                                                                                                                                                 LysGlySerGluSerCysAsnLeuPheLeuLysSerLeuLysGluTrpAsnTyrProLeu 80
                                                                                                                                                                                                                ATTCTGTCCTGTAAGGTGGCACAAGATCTAACAAGAGAACTGCTTAATGTTATTTTAAAA 301
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231404 MARC
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This sequence is from a Xenopus Gene Collection (XGC) library constructed by Aaron M. Zorn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Huckle,E., Taylor,R., Ashurst,J.L., Zorn,A.M. and Rogers,J. Sanger Xenopus tropicalis EST project 2001 (10_2001) Unpublished (2001)
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Silurana tropicalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sanger Xenopus tropicalis EST project TROPICALIS_SEQUENCE_ID: TGas028114.sp6
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1 (bases 1 to 728)
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /dev_stage="gastrila (stages 10.5-13 mixed)"
/lab_host="Escherichia coli XL1-blue"
/note="vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDN7
was oligo dT primed from 5ug of poly A+ RNA from stages
10-13 gastrulae. EcoRI-NotI cut cDNA was then ligated
into pCS107 with EcoRI at the 5' end and NotI at the 3'
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/clone="mor-""
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                                                                                                                                                                                                               GluLysValGlu---GlnAspAlaAlaArgGlyIleIleHisMetIleLeuLysLysGly 62
                                                                                                                                                                                                                                                 TTGGATGAACTATTACACACCAGAGTCCTGAACCAGGAGGAGGTGGAGATAGTAAGATGT
                                                                                                                 CCCCAGGCATGCCAAATTTGCATCAATCATATT
                                                                                                                                              SerGluSerCysAsnLeuPheLeuLysSerLeu 73
                                                                                                                                                                                CTGAAGGAGAAGAGGCTGTTTGTCCGTTCACTGGCCATGGGTACGATCAATGGCCTC
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Fax: 402 762 4390
                              BB199526
BB199526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Design and use of two pooled tissue EST discovery in swine Unpublished (2000)
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Sus scrofa
musculus
BB199526
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stone, R.T.
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Mammalia;
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BF080490.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       karyota; Metazoa; Chordata; Craniata; Vertebrata;
mmalia; Eutheria; Cetartiodactyla; Suina; Suidae;
(bases 1 to 571)
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/db_xref="taxon:9823"
/clone_lib="MARC 2PIG"
/tissue_type="pooled"
/lab_host="DH10B"
                 681 bp mRNA linear EST 31 RIKEN full-length enriched, 0 day neonate thymus cDNA clone A430015K19 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: Sal
Library made from pooled tissue from testis, ovary,
endometrium, hypothalamus, pltuitary, and placenta."
a 142 c 138 g 123 t
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Grosse,W.M., Bennett,G.A.,
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URL:http://genome.gsc.riken.go.jp/

URL:http://genome.gsc.riken.go.jp/

Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh

Carninci,P., Shibata,Y., Muramatsu,M. and Hayashizaki,Y.,

M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new

genes. Genome Res. . 10 (10), 1617-607 (2000)

wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,

watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura

A., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and

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Unpublished (2001)
On Jun 30, 2000 this sequence version replaced gi:8864479
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Mapping of 19032 mouse cDNAs on mouse chromosomes. J. Struct. Func. Genomics 2 pre, L72-L86 (2001)
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Laboratory for Genome Exploration Research Group, RIKEN Genomic
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA library was prepared and sequenced in Mouse Genome
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prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory RIKEN Division of Experimental Animal Research in Rik
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="thymus"
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                                                                          CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov Plate: LLCM524 row: p column: 19

High quality sequence stop: 747.
                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
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/clone="IMAGE:3838338"
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Creation of genome-wide protein expression libraries using random activation of gene expression
Nat. Biotechnol. 19 (5), 440-445 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                            RST9419 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
BG190354
BG190354.1 GI:13712041
EST.
Tel: 216 431 9900
Fax: 216 361 9596
Email: scain@athersys.com
High quality sequence stop:
                                                                                       Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave, Clev
                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 787)
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/lab_host="DH10B (phage-resistant)"
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                          Athersys, Inc.
3201 Carnegie Ave, Clevelan
Tel: 216 431 9900
Fax: 216 361 9596
Email: scain@athersys.com
                                                                                                                                                                       Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R., Cain, S., Leventhal, C., Thornton, M., Ramachandran, R., Whittington, J., Lerner, L., Costanzo, D., McElligott, K., Boozer, S., Mays, R., Smith, E., Veloso, N., Klika, A., Hess, J., Cothren, K., Lo, K., Offenbacher, J., Danzid, J. and Ducar, M.
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RST28980 Athersys RAGE Library
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/clone_lib="Athersys RAGE Library"
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/organism="Homo sapiens"
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                                      Athersys, Inc.
3201 Carnegie Ave, Clevelan
Tel: 216 431 9900
Fax: 216 361 9596
Email: scain@athersys.com
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Creation of genome-wide protein expression libraries using random activation of gene expression
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quality sequence stop: 473
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/cell_line="HT1080"
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BG188190.1
EST.
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1 (bases 1 to 812)

Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R., Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Boozer,S., Mays,R., Smith, E., Veloso,N., Kilka,A., Hess,J., Cothren,K., Lo,K., Offenbacher,J., Danzig,J. and Ducar,M.

Creation of genome-wide protein expression libraries using random activation of gene expression
Nat. Biotechnol. 19 (5), 440-445 (2001)
                                                3201 Carnegie Ave, Cleveland,
Tel: 216 431 9900
Fax: 216 361 9596
                                                                                       Athersys, Inc.
3201 Carnegie
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                                                                                                                         Contact: Scott J. Cain
                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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                                   Email: scain@athersys.com
                                                                                                                                               21227151
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quality sequence stop: !
Location/Qualifiers
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a 111 c 158 g 272 t 2 others
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/db_xref="taxon:9606"
/clone_ilb="Athersys RAGE Library"
/cell_line="HT1080"
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                                                                                                                                                                            Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC
                                                                                                                                                                                                                                           1 (bases 1 to 963)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
             High quality sequence stop: 629
Location/Qualifiers
                                                found through the I.M.A.G.E. Consortium/LLNL http://image.llnl.gov
Plate: LLAM10399 row: k column: 06
                                                                                                                                                                                                                              Unpublished (1999)
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Eukaryota; M
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                                                                                                                                                                                                                                                                                                       Mammalia; Eutheria;
                                                                                                    CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can
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a 113 c 156 g 273 t 1 others
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/db_xref="taxon:9606"
/clone_lib="Athersys RAGE Library"
/cell_line="HT1080"
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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EST 21-FEB-2001

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1 (bases 1 to 976)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
                                                    found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM10076 row: k column: 09
                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                           EST
                                                                                                                                                                                                                                                                                                                                                                                                                                          mRNA sequence.
BG028431
BG028431.1 GI:12417525
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                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                       human.
                                                                                                                CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLN DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information
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              quality sequence stop: 646.
Location/Qualifiers
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/clone_lib="NIH_MGC_93"
/clone_lib="NIH_MGC_93"
/tissue_type="transitional cell papilloma, cell line"
/note="Organ: bladder; Vector: pCMV-SPORT6; Site_1: Not!
Site_2: Sall; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.7 % Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
1144 c 231 g 262 t 1 others
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/db_xref="taxon:9606"
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                                                                                Lita Annenberg Hazen Genome Sequencing Center Cold Spring Harbor Laboratory PO Box 100, Cold Spring Harbor, NY 11724, USA
                                                                                                                                     Unpublished (2002)
Contact: W. Richard McCombie
                                                                                                                                                                                                      O'Shaughnessy,A.L., Palmer,L., McCombie,W.R., Baker,J.P., Bahret,A
Cunnius,D., Dedhia,N.N., de la Bastide,M., Katzenberger,F., King
,L., Kirchoff,K.A., Miller,B., Muller,S., Nascimento,L.U., Preston
,R.R., Shah,R.S., Spiegel,L.A., Zutavern,T., Santos,L. and Hannon
                                                                                                                                                                                                                                                                                                                                                                                           Tel: 516 367 8884 Fax: 516 367 8874
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                                                                                                                                                                                                                                                                                                                           Canis familiaris
                                                                                                                                                                                                                                                                                                                                                                             BQ235318.1 GI:20431194
                   Plate: hd56
                                 Email: mccombie@cshl.org
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Seq primer:
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/clone_lib="NIH_MGC_86"
/tissue_type="osteosaroma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: bone; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.533 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

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Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                        AV682308 GKB Homo sapiens cDNA clone GKBACA11 5',
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park,
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
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-Q-/cgn2_1/USPTC_spool/US09697089/runat_29012003_092754_19735/app_query.fasta_1.981
-DB=Tssued_Patents_NA -QFMT=fastap -SUFFIX=PQn:rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS-bits -START=1 -END=-1 -MATRIX-blosum62 -TRANS-human40.cdi
-LIST=45 -DCCALLGN=200 -TRR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE-LOCAL -OUTEMT=pto -NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER-US09697089_@CGN_11_137_@runat_29012003_092754_1935 -NCPU=6 -ICPU=3
-NO.XIPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -KGAPOP=10 -KGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
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US-08-569-749-1
PCT-US96-12860-1
US-09-205-204-1
US-09-212-971-7
US-08-800-929A-7
US-08-617-055A-7
US-08-5617-485-7
US-08-569-749-13
PCT-US96-12860-13
US-09-212-971-13
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: HE, ET AL.
TITLE OF INVENTION: Human Inhibitor of Apoptosis Gene
NUMBER OF SEQUENCES: 8
                                                                            ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,1
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INC
                                              TELECOMMUNICATION INFORMATION: TELEPHONE: 201-994-1700
                                                                                                                                                                           CLASSIFICATION: PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
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                                                                                                                                           FILING DATE:
                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE: 11 MA
                               TELEFAX:
                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                       SOFTWARE: WORD PERFECT 5.1
                                                                                                                                                                                                                                                                        OPERATING SYSTEM:
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PCT-US95-05922A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/08569749 Patent No. 6187557
                            INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                       REGISTRATION NUMBER: 24,774
REFERENCE/DOCKET NUMBER: A-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)781-1989
TELEPHONE: (415)38-3249
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                                                                                                                                                    CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Goeddel, David V
TITLE OF INVENTION: INHIBITORS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 1
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                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                               AGENT INFO....
Brezner, David J.
Brezner, David J.
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Best Local Similarity:
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                                                    REFERENCE/DOCKET NUMBER: A-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)781-1989
TELEFAX: (415)398-3249
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                       FILING DATE: 06 AUG CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
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APPLICATION NUMBER: PC'
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No.:
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                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
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                                                                                                                               NAME: Brezner, David J. REGISTRATION NUMBER: 24
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CITY: San Francisco
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                                                                                                                                                                           CLASSIFICATION:
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STRANDEDNESS:
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US-09-205-204-1
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LENGTH: 3532
TYPE: DNA
ORGANISM: Homo sapiens
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CURRENT FILING DATE: 1998-12-03
NUMBER OF SEQ ID NOS: 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: C. Frank Bennett
APPLICANT: Elizabeth J. Ackermann
APPLICANT: Lex M. Cowsert
TITLE OF INVENTION: ANTISENSE MODULATION OF CELLULAR INHIBITOR OF APOPTOSIS-1 EXPRESS
FILE REFERENCE: RTS-0020
                                                                                                                                                                                                                                                                                                                                        FEATURE:
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 1800 TATAAGAACTTA
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              LysGlnIleThrAspAspLeuPheValTrpAsnValLeuAsnArgGluGluValAsnIle 40
                                                           TTGTCATTAATTCGGAAGAACAGAATGGCTCTCTTTCAACAA-----TTGACATGTGTG
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APPLICANT: Tsang, Benjamin K
APPLICANT: Tsang, Benjamin K
APPLICANT: Pratt, Christine
TITLE OF INVENTION: DISEASE
TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AN
TITLE OF INVENTION: DISEASE
FILE REFERENCE: 07891/009002
CURRENT APPLICATION NUMBER: US/09/212,971B
CURRENT FILING DATE: 1998-12-16
EARLIER APPLICATION NUMBER: 60/017,354
EARLIER APPLICATION NUMBER: 60/030,590
EARLIER APPLICATION NUMBER: 09/030,590
EARLIER APPLICATION NUMBER: 09/030,590
EARLIER FILING DATE: 1996-01-14
EARLIER APPLICATION NUMBER: 09/030,590
EARLIER FILING DATE: 1997-02-13
NUMBER OF SEQ ID NOS: 17
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APPLICANT: Korneluk, Robert G
APPLICANT: MacKenzie, Alexander E
APPLICANT: Liston, Peter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FastSEQ for Windows Version
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TYPE: DNA
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2985 TATAAGAACTTA 2996
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                             PheGlnAspLeu 84
                                                             AAAGGAAATGCTGCGGCCAACATCTTCAAAAACTGTCTAAAAGAAATTGACTCTACATTG
                                                                             LysG1ySerG1uSerCysAsnLeuPheLeuLysSerLeuLysG1uTrpAsnTyrProLeu 80
                                                                                                                            IleCysCysGluLysValGluGlnAspAlaAlaArgGlyIleIleHisMetIleLeuLys 60
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                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 3732 base pair
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 60/017,354
FILING DATE: 26-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Blaker-Brady, Kristina
REGISTRATION NUMBER: 07891
                                                                                      2751 TTGTCATTAATTCGGAAGAACAGAATGGCTCTCTTTCAACAA-----TTGACATGTGTG
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PRIOR APPLICATION DATA:
APPLICATION UNMER: 60/030,590
FILING DATE: 14-NOV-1996
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TOPOLOGY: li
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Tsang, Benjamin K
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Best Local Similarity:
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Sequence 7, Application US/08511485 Patent No. 5919912 GENERAL INFORMATION:
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APPLICANT: Pratt, Christine
TITLE OF INVENTION: DETECTION AND
TITLE OF INVENTION: NAIP FOR THE
TITLE OF INVENTION: DISEASE
ETTE DEPERANCE. TO SECOND
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PRIOR FILING DATE: 1997-02-13
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 4
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APPLICANT: MacKenzie, Alexand
APPLICANT: Liston, Peter
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TYPE: DNA
ORGANISM: Homo sapiens
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DIAGNOSIS AND
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TREATMENT
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APPLICANT:

Baird, Stephen Korneluk, Robert G Mackenzie, Alexander E.

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US-08-569-749-13
; Sequence 13, Application US/08569749
; Patent No. 6187357
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Best Local Similarity:
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FILING DATE: 04-AUG-1995
FILING DATE: 04-AUG-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 200154
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 2580 base pairs
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEPAX: 617/542-8906
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STRANDEDNESS: both
TOPOLOGY: both
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Sequence 13, Application PC/TUS9612860
GENERAL INFORMATION:
APPLICANT: TULARIK, INC.
                                                                                       RESULT 10
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INFORMATION FOR SEQ ID NO:
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LENGTH: 2862 base pairs
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ATTORNEY/AGENT INFORMATION:
NAME: Brezner, David J.
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CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
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OF INVENTION:
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INHIBITORS OF APOPTOSIS
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NUMBER OF SEQUENCES:

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RESULT 11
US-09-212-971-13
; Sequence 13, Application US/09212971B
; Patent No. 6107041
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DB:
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GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G
APPLICANT: MacKenzie, Alexander
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INFORMATION FOR SEQ ID NO:
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REGISTON NUMBER: 24,774
REFERENCE/DOCKET NUMBER: A--
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)781-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 2862 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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CITY: San Francisco
STATE: Califactic
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FILING DATE: 06 AUG 1996
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LENGTH: 3151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE TITLE OF INVENTION: DISEASE FILE REFERENCE: 07891/009002
                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EARLIER APPLICATION NUMBER: 08/800,929
EARLIER FILING DATE: 1997-02-13
NUMBER OF SEO ID NOS: 17
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APPLICANT: Pratt, Christine
                                                                           APPLICANT: Baird, Stephen
APPLICANT: Tsang, Benjamin K
APPLICANT: Pratt, Christine
TITLE OF INVENTION: DETECTION ITTLE OF INVENTION: IAPS AND N
TITLE OF INVENTION: DISEASE
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ORGANISM: Mus
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No.:
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                                        CORRESPONDENCE ADDRESS
                                                         NUMBER OF SEQUENCES:
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STREET:
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  176 Federal Street
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                    Clark & Elbing LLP
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MEDIUM TYPE:

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Query Match:
DB:
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                                                                              GENERAL INFORMATION:
                                                                                            Sequence 13, Application US/09617053A Patent No. 6300492
                APPLICANT: Korneluk, Robert G
APPLICANT: MacKenzie, Alexand
APPLICANT: Liston, Peter
    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 3151 base pairs
TYPE: nucleic acid
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No.:
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PRIOR APPLICATION DARE: 60/030,590
PILING DATE: 14-NOV-1996
APPLICATION NUMBER: 60/017,354
APPLICATION NUMBER: 60/017,354
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ATTORNEY/AGENT INFORMATION:
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TOPOLOGY: lin
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REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/800,929A FILING DATE: 13-FEB-1997
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MacKenzie, Alexander E
Liston, Peter
Baird, Stephen
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; LENGTH: 3151
; TYPE: DNA
; ORGANISM: Mus n
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Best Local Similarity:
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APPLICANT: Pratt, Christine
TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
TITLE OF INVENTION: DISEASE
TITLE OF INVENTION: DISEASE
TILE REFERENCE: 07891/009003
CURRENT APPLICATION NUMBER: US/09/617,053A
CURRENT FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 08/800,929
PRIOR EILING DATE: 1997-02-13
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COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOTTWARE: Patentin Release #1.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield &
STREET: 600 Atlantic Avenue
                                                                                                                                                                                                                                                             APPLICANT: Talanian, Robert V.
APPLICANT: Dang, Leonard Luan Cao
APPLICANT: Walker, Nigel Pelham Clinton
APPLICANT: Ghayur, Tariq
TITLE OF INVENTION: ICE AND ICE-LIKE COMPOSITIONS
TITLE OF INVENTION: METHODS OF MAKING SAME
                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                               COUNTRY: US
ZIP: 02210
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Conservative:
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US-08-954-536-17

: Sequence 17, Application US/08954536

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DB:
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Best Local Similarity:
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                                                                                       APPLICANT:
APPLICANT:
            APPLICANT: Allen, Hamish
APPLICANT: Banerjee, Subhashis
APPLICANT: Paskind, Michael
TITLE OF INVENTION: Transgenic
TITLE OF INVENTION: Disrupted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/242,663A
FILING DATE: 12-MAY-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Janiuk, Anthony J.
REGISTRATION NUMBER: 29,809
REGISTRATION NUMBER: 29,809
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NUMBER OF SEQUENCES:
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TYPE: nucleic acid
STRANDEDNESS: single
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Li, Ping
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Transgenic No. 6100445human Animal Having Functionally
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Best Local Similarity:
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REFERENCE/DOCKET NUMBER: BBI-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEO ID NO: 17:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 08/3
FILING DATE: 14-OCT-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 STATE STREET, SUITE
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 301 ATGCAAGACTCTCAAGGA 318
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                             81 PheGlnAspLeuAsnGly
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TOPOLOGY: li
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION:
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Matches:
Conservative:
Mismatches:
Indels:
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Search completed: January 31, 2003, 15:16:34 Job time: 22.9209 secs

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Result
No.
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-MODEL-frame+_p2n.model -DEV=xlh
-O-/cgn2_1/USPTO_spool/US09697089/runat_29012003_092755_19800/app_query.fasta_1.981
-OB-published_Applications_NA -OFMT-fastap -SUFFIX=p2n.rnpb -MINMATCH=0.1
-DB-published_Applications_NA -OFMT-fastap -SUFFIX=p2n.rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALICN=200 -TRR_SCORE-pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE-LOCAL -OUTFMT-pto -NORM-ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER-US09697089_@CGN_1_1_48_@runat_29012003_092755_19800
-NCPD=6 -LCPU=3 -NO.XLPXY -NO.MMAP -LARGEDUERY -NEG_SCORES=0 -WAIT -LONGLOG
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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// cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
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// cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
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// cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
// cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
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Sequence 100, App
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ALIGNMENTS

RESULT 1 US-09-864-921-100

Sequence

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Application US/09864921

Patent No. US20020176853A1 GENERAL INFORMATION:

APPLICANT: Reed, John C.
APPLICANT: Pio, Frederick F.
APPLICANT: Godzik, Adam

APPLICANT:

Stehlik, Christian Damiano, Jason S.

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APPLICANT: Lee, Sug-Hyung
APPLICANT: Oliveira, Vasco A.
APPLICANT: Hayashi, Hideki
APPLICANT: Hayashi, Hideki
APPLICANT: Pawlowski, Krzysztof
TITLE OF INVENTION: No. US20020176853Alel Card Domain Containing
TITLE OF INVENTION: Polypeptides, Encoding Nucleic Acids, and Methods of Use
FILE REFERENCE: P-LJ 4752
CURRENT APPLICATION NUMBER: US/09/864,921
CURRENT FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: US 09/579,240
PRIOR APPLICATION NUMBER: US 09/586,347
PRIOR APPLICATION NUMBER: US 09/686,347
PRIOR FILING DATE: 2000-10-10-10
PRIOR FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 195
SOFTWARE: FastSEQ for Windows Version 4.0
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LENGTH:

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APPLICANT: Lee, Sug-Hyung
APPLICANT: Lee, Sug-Hyung
APPLICANT: Lee, Sug-Hyung
APPLICANT: Oliveira, Vasco A.
APPLICANT: Hayashi, Hideki
APPLICANT: Pawlowski, Krzysztof
TITLE OF INVENTION: No. US20020176853Alel Card Domain Containing
TITLE OF INVENTION: Polypeptides, Encoding Nucleic Acids, and Methods of U
FILE REFERENCE: P-LJ 4752
CURRENT APPLICATION NUMBER: US/09/864,921
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 09/579,240
PRIOR APPLICATION NUMBER: US 09/586,347
PRIOR APPLICATION NUMBER: US 09/686,347
PRIOR FILING DATE: 2000-10-10
PRIOR FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 195
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 102
LENCTH: 768
; ORGANISM: Homo sapien FEATURE:
; NAME/KEY: CDS
; LOCATION: (277)...(744)
US-09-864-921-102
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; LOCATION: (277)...(552)
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APPLICANT: Reed, J
APPLICANT: Pio, F
APPLICANT: GODZIK
APPLICANT: Stehli
APPLICANT: Damian
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                                                                                TYPE: DNA
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Damiano, Jason S.
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APPLICANT: Reed, John C.

APPLICANT: Pio, Frederick F.

APPLICANT: Godzik, Adam

APPLICANT: Stehlik, Christian

APPLICANT: Stehlik, Christian

APPLICANT: Stehlik, Christian

APPLICANT: Damiano, Jason S.

APPLICANT: Dee, Sug-Hyung

APPLICANT: Oliveira, Vasco A.

APPLICANT: Hayashi, Hideki

APPLICANT: Hayashi, Hideki

APPLICANT: Hayashi, Hideki

APPLICANT: Hayashi, Hideki

APPLICANT: Hayashi, Mo. US20020176853Alel Card Domain Containing

TITLE OF INVENTION: No. US20020176853Alel Card Domain Containing

TITLE OF INVENTION: Polypeptides, Encoding Nucleic Acids, and Metho:

FILE REFERENCE: P-LJ 4752

CURRENT APPLICATION NUMBER: US/09/864,921

CURRENT APPLICATION NUMBER: US 09/579,240

PRIOR APPLICATION NUMBER: US 09/579,240

PRIOR FILING DATE: 2000-05-24

PRIOR TILING DATE: 2000-05-24

PRIOR FILING DATE: 2000-01-03

PRIOR FILING DATE: 2001-03-14

NUMBER: US 60/275,980
                                                                                                                              TYPE: DNA
GRGANISM: Homo sapien
FEATURE:
NAME/KEY: CDS
LOCATION: (277)...(1353)
US-09-864-921-98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 98, Application US/09864921 Patent No. US20020176853A1
                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 195
SOFTWARE: FastSEQ for Windows Version 4.0
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3TH: 1395
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US-09-841-739-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 09/697,089
PRIOR FILING DATE: 2000-10-26
PRIOR APPLICATION NUMBER: US 60/161,822
PRIOR FILING DATE: 199-10-27
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE FILE REFERENCE: 07334-332001 CURRENT APPLICATION NUMBER: US/09/841,739
CURRENT FILING DATE: 2001-08-29
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                                                                                    ATTTGCTGCGAGAAGGTGGAGCAGGATGCTGCTAGAGGGGATCATTCACATGATTTTGAAA
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US-09-841-739-1
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                     APPLICANT: Reed, John C.
APPLICANT: Reed, John C.
APPLICANT: Pio, Frederick F.
APPLICANT: Godzik, Adam
APPLICANT: Stehlik, Christian
APPLICANT: Damiano, Jason S.
APPLICANT: Lee, Sug-Hyung
APPLICANT: Lee, Sug-Hyung
APPLICANT: Hayashi, Hideki
APPLICANT: Hayashi, Hideki
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SEQ ID NO 1
LENGTH: 3133
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                                                                                                                                                      Sequence 90 Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES FILE REFERENCE: 07334-329001 CURRENT APPLICATION NUMBER: US/09/841,739 CURRENT FILING DATE: 2001-08-29 PRIOR APPLICATION NUMBER: US 09/697,089 PRIOR APPLICATION NUMBER: US 09/697,089 PRIOR FILING DATE: 2000-10-26 PRIOR APPLICATION NUMBER: US 60/161,822 PRIOR APPLICATION NUMBER: US 60/161,822 PRIOR FILING DATE: 1999-10-27
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                APPLICANT:
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INVENTION: No. US20020176853Alel Card Domain Containing
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US-09-864-921-96
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                                                                                                                                                                                                                                                                                                                   Sequence 177, Application US/09864921 Patent No. US20020176853A1
APPLICANT: Paulowski, Krzysztof
TITLE OF INVENTION: No. US20020176853Alel Card Domain Containing
TITLE OF INVENTION: Polypeptides, Encoding Nucleic Acids, and Mc
FILE REFERENCE: p-LJ 4752
CURRENT APPLICATION NUMBER: US/09/864,921
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 09/579,240
PRIOR FILING DATE: 2000-05-24
PRIOR APPLICATION NUMBER: US 09/686,347
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PRIOR FILING DATE: 2000-05-24
PRIOR APPLICATION NUMBER: US 09/686,347
PRIOR FILING DATE: 2000-10-10
PRIOR APPLICATION NUMBER: US 60/275,980
PRIOR FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 195
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CURRENT FILING DATE: 2001-05-23
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Oliveira, Vasco A.
Hayashi, Hideki
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Damiano, Jason S.
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US-09-864-921-177
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PRIOR FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 195
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 177
LENGTH: 261
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                            Sequence 6, Application US/09841739
Patent No. US20020034784A1
GENERAL INFORMATION:
APPLICANT: Bertin, John
                                                                                                                                                                                 SEQ ID NO 6
                                                                                                                                                                                                          CURRENT FILING DATE: 2001-08-29
PRIOR APPLICATION NUMBER: US 09/697,089
PRIOR FILING DATE: 2000-10-26
PRIOR APPLICATION NUMBER: US 60/161,822
PRIOR FILING DATE: 1999-10-27
NUMBER OF SEQ ID NOS: 16
                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES FILE REFERENCE: 07334-329001 CURRENT APPLICATION NUMBER: US/09/841,739 CURRENT FILING DATE: 2001-08-29
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NAME/KEY: CDS
LOCATION: (1).
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                                                                                                                                   TYPE: DNA
ORGANISM: Homo
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Query Match:
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US-09-841-739-4
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TITLE OF INVENTION: NOVEL MOLECULES OF THE CAP
FILE REFERENCE: 07334-329001
FILE REFERENCE: 07334-329001
CURRENT APPLICATION NUMBER: US/09/841,739
CURRENT FILING DATE: 2001-08-29
PRIOR APPLICATION NUMBER: US 09/697,089
PRIOR FILING DATE: 2000-10-26
PRIOR APPLICATION NUMBER: US 60/161,822
PRIOR FILING DATE: 1999-10-27
NUMBER OF SEQ ID NOS: 16
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SEQ ID NO 4
LENGTH: 3615
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ORGANISM: Homo
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                                                                                                                                      ; GENERAL INFORMATION:
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                                                                                                                                                   Sequence 14, Application US/09917265 Patent No. US20020052030A1
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SEQ
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                               APPLICANT: Wonderling, Ramani S.
APPLICANT: BOTOUGHS, KAIEN L.
TITLE OF INVENTION: CANINE AND FELINE PROTEINS,
FILE REFERENCE: IM-5
CURRENT APPLICATION NUMBER: US/09/917,265
CURRENT FILING DATE: 2001-07-27
PRIOR APPLICATION NUMBER: 60/223,016
PRIOR FILING DATE: 2000-08-04
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PRIOR FILING DATE: 1999-10-27
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 4
           NUMBER OF SEQ ID NOS: 109
SOFTWARE: PatentIn version
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ORGANISM:
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US-09-697-089-2_COPY_1_88 (1-88) x US-09-841-739-12 (1-3615)
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TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES
FILE REFERENCE: 07334-329001
CURRENT APPLICATION NUMBER: US/09/841,739
CURRENT FILING DATE: 2001-08-29
PRIOR APPLICATION NUMBER: US 09/697,089
PRIOR PILING DATE: 2000-10-26
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US-09-917-265-16/c
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patent No. US20020052030A1
GENERAL INFORMATION:
APPLICANT: Wonderling, Ramani S.
APPLICANT: BOTOUGHS, KATEN L.
TITLE OF INVENTION: CANINE AND FELINE PROTEINS,
FILE REFERENCE: IM-5
                                                                                                                                                                                                                                                     SOFTWARE: PatentIn version 3.1
SEQ ID NO 16
LENGTH: 1233
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CURRENT FILING DATE: 2001-07-27
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LOCATION: (1)..(12
OTHER INFORMATION:
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US-09-917-265-17
; Sequence 17, Application US/09917265
; Patent No. US20020052030A1
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SOFTWARE: PatentIn version 3.1
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CURRENT FILING DATE: 2001-07-27
PRIOR APPLICATION NUMBER: 60/223,016
PRIOR FILING DATE: 2000-08-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Wonderling, Ramani S.
APPLICANT: Boroughs, Karen L.
TITLE OF INVENTION: CANINE AND FELINE PROTEINS,
FILE REFERENCE: IM-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 52
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: CDS
LOCATION: (18)..(5
OTHER INFORMATION:
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; SEQ ID NO 19
; LENGTH: 526
; TYPE: DNA
; ORGANISM: Felis catus
US-09-917-265-19
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Query Match:
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Sequence 19, Application US/09917265

Patent No. US20020052030A1

GENERAL INFORMATION:
APPLICANT: Wonderling, Ramani S.
APPLICANT: Boroughs, Karen L.
TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC
FILE REFERENCE: IN-5
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                                                                                                                     CURRENT APPLICATION NUMBER: US/09/917,265
CURRENT FILING DATE: 2001-07-27
PRIOR APPLICATION NUMBER: 60/223,016
PRIOR FILING DATE: 2000-08-04
NUMBER OF SEQ ID NOS: 109
SOFTMARE: Patentin version 3.1
SEQ ID NO 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/917,265
CURRENT FILING DATE: 2001-07-27
PRIOR APPLICATION NUMBER: 60/223,016
PRIOR FILING DATE: 2000-08-04
NUMBER OF SEQ ID NOS: 109
SOFTWARE: Patentin version 3.1
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APPLICANT: Boroughs, Karen L.
TITLE OF INVENTION: CANINE AND FELINE PROTEINS,
FILE REFERENCE: IM-5
                                                                  TYPE: DNA
ORGANISM: Felis catus
NAME/KEY: CDS
LOCATION: (1)..(1230)
OTHER INFORMATION:
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-O-/cgn2_1/USPTO_spool/US09697089/runat_29012003_092754_19749/app_query.fasta_1.981
-DB-Pending_Patents_NA_Main -QFWT-fastap -SUFFIX-p2n.rnpm -MINMATCH-0.1
-LOOPCL-0 -LOOPEXT-0 -UNITS-bits -START-1 -END--1 -MATRIX-blosum62
-TRANS-human40.cdi -LIST-45 -DOCALIGN-200 -THR_SCORE-pct -THR_MAX-100
-THR_MIN-0 -ALIGN-15 -MODE-LOCAL -OUTFMT-pto -NORM-ext -HEAPSIZE-500 -MINLEN-0
-MAXLEN-200000000 -USER-US09697089_@CGN_1_1_3083_@runat_29012003_092754_19749
-NCPU-6 -ICPU-3 -NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES-0 -WAIT -LONGLOG
-DEV_TIMEOUT-120 -WARN_TIMEOUT-30 -THREADS-1 -XGAPOP-10 -XGAPOXT-0.5 -FGAPOP-6
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| 6 | 5 | 4 | ω | 2 | 1 | Result |
|-------------------|-------------------|-------------------|-------------------|-------------------|---------------------|--------------------------|
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| 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | Query Match Length DB ID |
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| Sequence 3, Appli | Sequence 3, Appli | Sequence 3, Appli | Sequence 98, Appl | Sequence 102, App | Sequence 100, App | Description |

```
GENERAL INFORMATION C.

APPLICANT: Reed, John C.

APPLICANT: Pio, Frederick F.

APPLICANT: Godzik, Adam

APPLICANT: Godzik, Adam

APPLICANT: Godzik, Adam

APPLICANT: Stebhlik, Christian

APPLICANT: Damiano, Jason S.

APPLICANT: Lee, Sug-Hyung

APPLICANT: Lee, Sug-Hyung

APPLICANT: Pawlowski, Krzysztof

FITLE OF INVENTION: Novel Card Domain Containing

TITLE OF INVENTION: Polypeptides, Encoding Nucleic Acids, and

FILE REFERENCE: p-LJ 4752

CURRENT PRILING DATE: 2001-05-23

PRIOR APPLICATION NUMBER: US 09/579,240

PRIOR APPLICATION NUMBER: US 09/579,240

PRIOR FILING DATE: 2000-05-24

PRIOR APPLICATION NUMBER: US 09/686,347

PRIOR FILING DATE: 2000-10-10

PRIOR FILING DATE: 2001-05-14

NUMBER OF SED ID NOS: 195

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 100

LENGTH: 578

TYPE: DNA

ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-864-921-100; Sequence 100, A
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US-09-697-089-1
US-09-841-739-1
US-10-156-733-14
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APPLICANT: Coultry, Four-
APPLICANT: Lee, Sug-Hyung
APPLICANT: Lee, Sug-Hyung
APPLICANT: Lee, Sug-Hyung
APPLICANT: Oliveira, Vasco A.
APPLICANT: Hayashi, Hideki
APPLICANT: Hayashi, Krzysztof
APPLICANT: Pawlowski, Krzysztof
APPLICANT: Pawlowski, Krzysztof
APPLICANT: Pawlowski, Krzysztof
FITLE OF INVENTION: Polypeptides, Encoding Nucleic
FILE REFERENCE: P-LJ 4752
CURRENT APPLICATION NUMBER: US/09/864,921
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 09/579,240
PRIOR FILING DATE: 2000-05-24
PRIOR FILING DATE: 2000-10-10
PRIOR APPLICATION NUMBER: US 09/686,347
PRIOR APPLICATION NUMBER: US 09/686,347
PRIOR APPLICATION NUMBER: US 60/275,980
PRIOR APPLICATION NUMBER: US 60/275,980
PRIOR FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 195
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 102
LENGTH: 768
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Query Match:
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; NAME/KEY: CDS
; LOCATION: (277)...(552)
US-09-864-921-100
Alignment Scores:
Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Reed, John C.
APPLICANT: Pio, Frederick F.
APPLICANT: Godzik, Adam
APPLICANT: Stehlik, Christian
APPLICANT: Damiano, Jason S.
APPLICANT: Lee, Sug-Hyung
APPLICANT: Lee, Sug-Hyung
APPLICANT: Hayashi, Hideki
APPLICANT: Hayashi, Hideki
APPLICANT: Pawlowski, Krzyszto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 102, Applic GENERAL INFORMATION:
                                                                                   TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: CDS
LOCATION: (277)...(744)
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Query Match:
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CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 09/579,240
PRIOR FILING DATE: 2000-05-24
PRIOR APPLICATION NUMBER: US 09/686,347
PRIOR FILING DATE: 2000-10-10
PRIOR APPLICATION NUMBER: US 60/275,980
PRIOR FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 195
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 98, Application US/09864921 GENERAL INFORMATION:
                                                                                                                                                                                                                                    SEQ ID NO 98
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APPLICANT: Pawlowski, Krzysztof
TITLE OF INVENTION: Novel Card Domain Containing
TITLE OF INVENTION: Polypeptides, Encoding Nucle
FILE REFERENCE: P-LJ 4752
                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                               LENGTH: 1395
TYPE: DNA
ORGANISM: Homo
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  MetAsnPheIleLysAspAsnSerArgAlaLeuIleGlnArgMetGlyMetThrValIle
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Oliveira, Vasco A.
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Stehlik, Christian
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; LENGTH: 3072
; TYPE: DNA
; ORGANISM: Homo s
PCT-US00-29643-3
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Best Local Similarity:
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TITLE OF INVENTION: NOVEL MOLECULES OF THE C
TITLE OF INVENTION: PROTEIN FAMILY AND USES
FILE REFERENCE: 07334-136W01
CURRENT APPLICATION NUMBER: PCT/US00/29643
CURRENT FILING DATE: 2000-10-26
PRIOR APPLICATION NUMBER: US 60/161,822
PRIOR FILING DATE: 1999-10-27
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Best Local Similarity:
Query Match:
DB:
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; ORGANISM: Homo
US-09-841-739-3
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US-09-841-739-3
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  Best Local Similarity:
                 Percent Similarity:
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                                                                                                                                              SEQ ID NO 3
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LENGTH: 3072
                                                                                                                                                       APPLICANT: Bertin, John
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
FILE REFERENCE: 07334-32901
CURRENT APPLICATION NUMBER: US/09/841,739
CURRENT FILING DATE: 2001-08-29
PRIOR APPLICATION NUMBER: US 09/697,089
PRIOR FILING DATE: 2000-10-26
PRIOR FILING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: US 60/161,822
PRIOR FILING DATE: 1999-10-27
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 4.0
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TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
FILE REFERENCE: 07334-136001
CURRENT APPLICATION NUMBER: US/09/697,089
CURRENT FILING DATE: 2000-10-26
PRIOR APPLICATION NUMBER: US 60/161,822
PRIOR APPLICATION NUMBER: US 60/161,822
NUMBER OF SEQ ID NOS: 12
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TITLE OF INVENTION: FACTOR
FILE REFERENCE: 480140.477
CURRENT APPLICATION NUMBER: US/10/
CURRENT FILLING DATE: 2002-05-24
NUMBER OF SEQ ID NOS: 14
SOFTMARE: FASTSEQ for Windows Vers
SEQ ID NO 1
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US-10-156-733-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 3075
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RESULT 8 PCT-US00-29643-1

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PCT-US00-29643-1
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US-09-697-089-1
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TITLE OF INVENTION: NOVEL MOLECULES OF THE CAR
TITLE OF INVENTION: PROTEIN FAMILY AND USES TH
FILE REFERENCE: 07334-136W01
CURRENT APPLICATION NUMBER: PCT/US00/29643
CURRENT FILING DATE: 2000-10-26
PRIOR APPLICATION NUMBER: US 60/161,822
PRIOR FILING DATE: 1999-10-27
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FASTSEQ for Windows Version 4.0
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            NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
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                                                          APPLICANT: Robison, Keith E.

TITLE OF INVENTION: NOVEL MCLEULES OF THE CARD-RELATED
TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
FILE REFERENCE: 07334-136001
CURRENT APPLICATION NUMBER: US/09/697,089
CURRENT FILING DATE: 2000-10-26
PRIOR APPLICATION NUMBER: US 60/161,822
PRIOR FILING DATE: 1999-10-27
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LOCATION: (36)
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LENGTH: 3133
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US-09-697-089-1
                                          US-09-697-089-2_COPY_1_88 (1-88) x US-09-841-739-1
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LENGTH: 3133
TYPE: DNA
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TITLE OF INVENTION: NOVEL MOLECULES OF THI
FILE REFERENCE: 0734-329001
CURRENT APPLICATION NUMBER: US/09/841,739
CURRENT FILING DATE: 2001-08-29
                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 09/697,089 PRIOR FILING DATE: 2000-10-26
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US-10-156-733-14
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Sequence 96, Application US/09864921
GENERAL INFORMATION:
APPLICANT: Reed, John C.
APPLICANT: Pio, Frederick F.
APPLICANT: Godzik, Adam
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GENERAL INFORMATION:
APPLICANT: Alnemri, Emad S.
TITLE OF INVENTION: IPAF, AN ICE-PROTITLE OF INVENTION: FACTOR
FILE REFERENCE: 480140.477
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14
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US-09-491-404-1319; Sequence 1319; A
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Best Local Similarity:
APPLICANT: Tang, Yuanhua T.
APPLICANT: Tillinghast, John
APPLICANT: Sinku, Ankura
APPLICANT: Sinku, Ankura
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: Novel Contigs Obtained
TITLE OF INVENTION: From Various Libraries
FILE REFERENCE: 785
CURRENT APPLICATION NUMBER: US/09/491,404
CURRENT FILING DATE: 2000-01-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-697-089-2_COPY_1_88 (1-88) x US-09-864-921-96 (1-3396)
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LENGTH: 3396
TYPE: DNA
                                                                                                                                                                                                 GENERAL INFORMATION:
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APPLICANT:
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PRIOR FILING DATE: 2000-05-24
PRIOR APPLICATION NUMBER: US 09/686,347
PRIOR FILING DATE: 2000-10-10
PRIOR APPLICATION NUMBER: US 60/275,980
PRIOR FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 195
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APPLICANT: Oliveira, Vasco A.
APPLICANT: Hayashi, Hideki
APPLICANT: Hayashi, Hideki
APPLICANT: Pawlowski, Krzysstof
TITLE OF INVENTION: Novel Card Domain Containing
TITLE OF INVENTION: Polypeptides, Encoding Nucl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/864,921 CURRENT FILING DATE: 2001-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Polypeptides, Encoding FILE REFERENCE: P-LJ 4752
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NAME/KEY: CDS
LOCATION: (277)...(3348)
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                                                                                                                                                                                                                   Application
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                                                           From Various Libraries
                                                                               Radoje T.
Novel Contigs Obtained
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Matches:
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Indels:
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SEQ ID NOS:

OTHER INFORMATION: MIWGSGKCKALTKFKFVFFLRLSRAQGGLFETLCDQLLDIPGTIR, Run with Signal

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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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CATION: (679)...(3279);
COTHER INFORMATION: simila
COTHER INFORMATION: Run wi
US-09-491-404-1319
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                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/922,279
CURRENT FILING DATE: 2001-08-03
PRIOR APPLICATION NUMBER: 09/491,404
PRIOR FILING DATE: 2001-01-25
NUMBER OF SEQ ID NOS: 3796
SOFTWARE: pt_SP_genes Version 1.0
SEQ ID NO 1319
LENGTH: 3545
THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: Novel Contigs Obtained
TITLE OF INVENTION: From Various Libraries
FILE REFERENCE: 785
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APPLICANT: Tillinghast, John
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FEATURE:
REATURE:
NAME/KEY: sig_peptide
LOCATION: (781)...(916)
OTHER INFORMATION: this location contains the signal peptide sequence,
OTHER INFORMATION: MLMGSGKCKALTKFKFVFFLRLSRAQGGLFETLCDQLLDIPGTIR, Run with SignalP
                                                                                                                           TYPE: DNA ORGANISM: Homo sapiens
NAME/KEY: sig_peptide
LOCATION: (781)...(916)
OTHER INFORMATION: this location contains the signal peptide sequence.
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                                                                                                    FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Liu, Chenghua
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Matches:
Conservative:
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Alignment Scores: Pred. No.:
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Sequence 1319, Application U
GENERAL INFORMATION:
APPLICANT: Tang, Yuanhua T.
APPLICANT: Tillinghast, Jo
APPLICANT: Sinku, Ankura
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Best Local Similarity:
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                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 3796
SOFTWARE: pt_Sp_genes Version 1.0
SEQ ID NO 1319
LENGTH: 3545
                                                                                                                                                                                                                                                                                                                                            APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: Novel Contigs Obtained
TITLE OF INVENTION: From Various Libraries
FILE REFERENCE: 785
FULL REFERENCE: 785
CURRENT APPLICATION NUMBER: US/09/922,279A
CURRENT FILING DATE: 2001-08-03
PRIOR APPLICATION NUMBER: 09/491,404
PRIOR ETLING DATE: 2000-01-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                  NAME/KEY: misc_feature
LOCATION: (679)...(3279)
OTHER INFORMATION: simila
OTHER INFORMATION: Run w.
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LOCATION: (679)...(3279)
OTHER INFORMATION: similar t
OTHER INFORMATION: Run with
                                                                                                                                                     NAME/KEY: sig_peptide
LOCATION: (781)...(916)
OTHER INFORMATION: MLWGSGKCKALTKFKFVFFLRLSRAQGGLFETLCDQLLDIPGTIR, Run
OTHER INFORMATION: MLWGSGKCKALTKFKFVFFLRLSRAQGGLFETLCDQLLDIPGTIR, Run
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Perfect score:
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-Q=/cgn2_1/USPf0_spool/US99697089/runat_29012003_092755_19775/app_query.fasta_1.981
-DQ=/cgn2_1/USPf0_spool/US99697089/runat_29012003_092755_19775/app_query.fasta_1.981
-DB=Pending_Patents_NA_New -QPMT=fastap -SUFFIX=p2n.rnpn -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANNS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE-LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER-US09697089_eCGN_1_1_91_erunat_29012003_092755_19775
-NCPU=6 -ICPU=3 -NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG
-DEV_TIMEDUT=120 -WARN_TIMEDUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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Maximum Match 10
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length: 2000000000
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Match
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1: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq:*

2: /cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq:*

3: /cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq:*

4: /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*

5: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:*

6: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:*

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US-10-276-774-1303
PCT-US02-04915-82
US-10-311-035-36
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| •••• | equence 42, Apequence 14339, equence 4197, | • | Sequence 6860, Ap Sequence 6860, Ap Sequence 6859, Ap Sequence 6859, Ap Sequence 238, App | 279, 279, 40, 95, A | 1335 1147 1147 1147 1076 31, 1436 |

ALIGNMENTS

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Percent Similarity:
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SEQ ID NO 1
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                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Thomas Jefferson University
APPLICANT: Alhemri, Emad S.
TITLE OF INVENTION: IPAF, AN ICE-PROTEASE ACTIVATING
TITLE OF INVENTION: FACTOR
FILE REFERENCE: 480140.4077EC
CURRENT APPLICATION NUMBER: PCT/US02/21946A
CURRENT FILING DATE: 2002-05-24
                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                    NAME/KEY: CDS
LOCATION: (1)
                                                                                                                                                                                                                                                    FEATURE:
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Scores:

    Application PC/TUS0221946A

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; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-USO2-21946A-14
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GENERAL INFORMATION:
APPLICANT: Thomas Jefferson University
APPLICANT: Alnemri, Emad S.
TITLE OF INVENTION: ITAF, AN ICE-PROTEASE ACTIVATING
TITLE OF INVENTION: FACTOR
TITLE OF INVENTION: FACTOR
FILE REFERENCE: 480140.477PC
CURRENT APPLICATION NUMBER: PCT/US02/21946A
CURRENT APPLICATION NUMBER: PCT/US02/21946A
CURRENT FILING DATE: 2002-05-24
NUMBER OF SEQ ID NOS: 14
           Sequence 111, Application US/10276781
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
APPLICANT: Tang et al.
TITLE
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US-10-276-781-111
Percent Similarity:
Best Local Similarity:
                                                            Alignment Scores:
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Query Match:
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LENGTH: 3545
                                                                                                                                                                                                               SEQ ID NO 1
                                                                                                                                                                                                                                                   APPLICANT: He, et al.

TITLE OF INVENTION: Human Inhibitor of Apotosis of File Reference: pri65plD1

CURRENT APPLICATION NUMBER: US/10/323,643

CURRENT FILING DATE: 2002-12-20

PRIOR APPLICATION NUMBER: 08/464,588

PRIOR FILING DATE: 1995-06-05

PRIOR APPLICATION NUMBER: PCT/US95/05922

PRIOR APPLICATION NUMBER: PCT/US95/05922

PRIOR FILING DATE: 1995-05-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: 21272-018 (785 contig)
CURRENT APPLICATION NUMBER: US/10/276,781
CURRENT FILING DATE: 2002-11-18
PRIOR APPLICATION NUMBER: 09/491,404
PRIOR FILING DATE: 2000-01-25
NUMBER OF SEQ ID NOS: 2018
                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 10
                                                                                                                                                                                                                             SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
                                                                                                        OTHER
                                                                                                                                                                  ORGANISM: Homo
                                                                                                                      NAME/KEY: CDS
LOCATION: (10)
                                                                                                                                                     FEATURE:
                                                                                                                                                                                   TYPE: DNA
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                                                                                                                                                                                                                             PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                          Application US/10323643
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DB:
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LENGTH: 429
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CURRENT APPLICATION NUMBER: US/10/276,774
CURRENT FILING DATE: 2002-11-18
PRIOR APPLICATION NUMBER: 09/560,875
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 2000-04-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Hyseq, Inc.
APPLICANT: Tang, Y, Tom et al
TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 2700 SOFTWARE: Custom
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PRIOR FILING DATE: 2000-02-03
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                            Leu
ATT 412
                                                            ATCGATAAGGCCCGAGATTTGCTTGACTCTGTTATTCGGAAAGGGGCACGGGCATGTGAA 409
                                                                                         ---AspAlaAlaArgGlyIleIleHisMetIleLeuLysLysGlySerGluSerCysAsn 67
                                                                                                                                                                                          CGGCTGCTTATCAATTCATTGGGTGAAGGTACAATAAATGGCTTACTGGATGAATTATTG 289
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US-10-311-035-36
; Sequence 36, Application US/10311035
; GENERAL INFORMATION:
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PRIOR FILING DATE: 2001-02-14
PRIOR APPLICATION NUMBER: US 09/791,390
PRIOR FILING DATE: 2001-02-22
PRIOR APPLICATION NUMBER: US 60/285,475
PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: US 60/310,025
PRIOR FILING DATE: 2001-08-03
PRIOR APPLICATION NUMBER: US 60/350,666
PRIOR APPLICATION NUMBER: US 60/350,666
PRIOR FILING DATE: 2001-11-13
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LENGTH: 5059
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TITLE OF INVENTION: Methods of Diagnosis of Anglogenesis, Compositions and
TITLE OF INVENTION: Methods of Screening for Anglogenesis Modulators
FILE REFERENCE: 018501-006200PC
CURRENT APPLICATION NUMBER: PCT/US02/04915
CURRENT FILING DATE: 2002-02-14
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APPLICANT
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                   APPLICANT:
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                                                                                                                                                                                                                                                                                                                            63
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            ELLIOTT, Vicki
GANDHI, Ameena R.
LAL, Preeti
AU-YOUNG, Janice
TRIBOULEY, Catherine M
DELEGEANE, Angelo M.
                                                                                                                                                          INCYTE GENOMICS,
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Watson, Susan R.
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BAUGHN, Mariah
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NGUYEN, Danniel B.

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RESULT 8
US-09-724-676-11471
; Sequence 11471, Application
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Query Match:
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; OTHER INFORMATION: Inc:
US-10-311-035-36
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PRIOR FILING DATE: 2000-06-16; 2000-06-22; 2000-06-29; 2000-07-07; 2000-07-14
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PERL PROGRAM
SEQ ID NO 36
LENGTH: 549
                                                                                                                        GENERAL INFORMATION:
SEQ ID NO 11471
                         APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
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            SOFTWARE: PatentIn
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FILE REFERENCE: PI-0123 PCT
CURRENT APPLICATION NUMBER: US/10/311,035
CURRENT FILING DATE: 2002-12-10
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; NAME/KEY: misc_feature
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; OTHER INFORMATION: n is
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SEQ ID NO 11471
LENGTH: 542
TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                    APPLICANT: Compugen LTD TITLE OF INVENTION: Variants of alternative FILE REFERENCE: 129181.4 Compugen CURRENT APPLICATION NUMBER: US/09/724,676A CURRENT FILING DATE: 2000-11-28 NUMBER OF SEQ ID NOS: 97222
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GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative
FILE REFERENCE: 129181.4 Compugen
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CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 11469
LENGTH: 358
                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (20)...(20)
OTHER INFORMATION: n is
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OTHER INFORMATION:
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                                                                                          CTGAAGGAGAAAGCTGTTTATCCATTCCATGGGTGAAGGTACAATAAATGGCTTA 122
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US-09-513-999c-1335

Sequence 1335, Application US/09513999C

GENERAL INFORMATION:

APPLICANT: Dumas Milne Edwards, J.B.

APPLICANT: Duclert, A.

APPLICANT: Duclert, A.

APPLICANT: Giordano, J.Y.

TITLE OF INVENTION: Expressed Sequence Tags and Enc.

FILE REFERENCE: 59.US2.REG

CURRENT APPLICATION NUMBER: US/09/513,999C

CURRENT FILING DATE: 2000-02-24
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SEQ ID NO 11469
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CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
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PRIOR APPLICATION NUMBER: US PRIOR FILING DATE: 1999-02-26

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GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEO ID NOS: 97222
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LENGTH: 362
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SOFTWARE: Patent.pm
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; APPLICANT: Compugen LTD; TITLE OF INVENTION: Variants of alternative sp; FIITE REFERENCE: 129181.4 Compugen; CURRENT APPLICATION NUMBER: US/09/724,676A; CURRENT FILING DATE: 2000-11-28; NUMBER OF SEQ ID NOS: 97222; SOFTWARE: PatentIn version 3.2; SEQ ID NO 11470; LENGTH: 479
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CURRENT APPLICATION NUMBER: US/10/305,720 CURRENT FILING DATE: 2002-11-26 PRIOR APPLICATION NUMBER: 09/016,434 PRIOR FILING DATE: 1998-01-30 NUMBER OF SEQ ID NOS: 1490 SOFTWARE: PERL Program
                                                                                               APPLICANT: Au-Young, Janice K.; Seilhame TITLE OF INVENTION: Composition for the FILE REFERENCE: PA-0002-1 CON
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OTHER INFORMATION: n is a,c,g,
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LENGTH: 2563
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: GenBank ID No: g1160974
US-10-305-720-1076
Search completed: January 31, 2003, 18:02:50 Job time: 85.778 secs
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-DB-GenEmb1 -QEMT=fastap -SUFFIX-p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=b1ts -START=1 -END=-1 -MATRIX-b1osum62 -TRANS-human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE-pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER-US09697089_GCGN_1_3568_@runat_29012003_092753_19716 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARR_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPEXT=7
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41: em_htgo_mus:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. C C 0.000 C C 0 0 236.55 23 Score Query Match 82976 131078 155306 155308 155809 155974 168814 190871 6829 117791 168388 206808 41613 4752 4815 Length DВ 10 AC116741) AF361881) AF131205 AF242431S1 AC114378 AC093971 AC044797 HSNAIP1 AF135494 A64529 AX335820 HSU19251 A64510 A64531 AC005031 HSU80017 AC010272 AC109487 AC0123169 AC022113 AY032589 AY0325391 AK095467 BC031555 AX3158091 AY3276061 CNS01DS3 AC010968 AC101793 AB048534 E23944 AF242433S1 AF135490 AF102871 AF135489 AF007769 AF242431S2 E24989 E38321 AX318174 Ĭ U19251 Homo Sapien A64510 Sequence 2 A64531 Sequence 23 AC005031 Homo sapien AC010272 Homo sapien AC010272 Homo sapi AC012369 Homo sapi AC012369 Homo sapi AC012379 Homo sapi AC012379 Homo sapi AC012379 Homo sapi AC014797 Homo sapi AC014797 Homo sapien AF135494 Mus muscu AF242431 Mus muscu AF242433 Mus muscu AF344433 Mus muscu AF135490 Mus muscu AF135490 Mus muscu AF135490 Mus muscu AF135490 Mus muscu AF135490 Mus muscu AF135490 Mus muscu AF135490 Mus muscu AF135489 Mus muscu AF135489 Mus muscu AF135480 Mus muscu AF135480 Mus muscu AF135480 Mus muscu AF135480 Mus muscu AK095467 Homo sapi BC031555 Homo sapi AX318091 Sequence AY027787 Homo sapi AL121653 BAC seque AC010968 Homo sapi AC101793 Mus muscu AB048534 Homo sapi E23944 Excessive o E24990 Apoptosis-i A64509 Sequence 1 E23943 Excessive o E24989 Apoptosis-i E38321 Monoclonal AX318174 Sequence AY032589 Homo sap AY035391 Homo sap A64529 Sequence 21 AX335820 Sequence Description . Mus muscu 1 Rattus no

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LSRAQGGLFETLCDQLLDIPGTIRKQTFMAMLLKLRQRVLFLLDGYNEFKPQNCPEIE
ALIKENHRFKNNVIVTTTECLRHIRGFGALTAVGDMTEDSAQALIREVLIKELAEG
LLLQIQKSRCLRNLMKTPLFVVITCAIQMGESEFHSHTQTTLFHTFYDLLIQKNKHKH
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228 c 217 g 209 t
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STKEFLPDPALVRKLSQVLSKLTFLQEARLVGWQFDDDDLSVITGAFKLVTA"
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                                   Direct Submission
Submitted (16-MAY-2001) Microbiology and Immunology, Thomas Submitted University, 233 S. 10th Street, Philadelphia, PA
                                                                                                                                     Poyet, J.L., Srinivasula, S.M., Tnani, M., Razmara, Fernandes-Alnemri, T. and Alnemri, E.S. Identification of Ipaf, a human caspase-1-activa related to Apaf-1
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                                                                             Poyet, J.-L., Alnemri, E.S.
                                                                                                                     J. Biol. Chem.
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STKEFLPDPALVRKLSQVLSKLTFLQEARLVGWQFDDDDLSVITGAFKLVTA'
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LQSPCIIEGESGKGKSTLLQRIAMLWGSGKCKALTKFKFVFFLRLSRAQGGLFETLCD
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Matches:
Conservative:
Mismatches:
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CAGAGGGTTCTTTTCCTTCTTGATGGCTACAATGAATTCAAGCCCCAGAACTGCCCAGAA GlnArgValLeuPheLeuLeuAspGlyTyrAsnGluPheLysProGlnAsnCysProGlu

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ThrGluCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMet 140 984

ThrGluAspSerAlaGlnAlaLeuIleArgGluValLeuIleLysGluLeuAlaGluGly 160 ACAGAAGACAGCGCCCCAGGCTCTCATCCGAGAAGTGCTGATCAAGGAGCTTGCTGAAGGC

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TITLE
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                21 ArgIleAlaMetLeuTrpGlySerGlyLysCysLysAlaLeuThrLysPheLysPheVal
                                                                                                       1 LeuGlnSerProCysIleIleGluGlyGluSerGlyLysGlyLysSerThrLeuLeuGln
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CGAATTGCCATGCTCTGGGGCTCCGGAAAGTGCAAAGTCTGACCAAGTTCAAATTCGTC
                                                                                   CTTCAGAGCCCCTGCATCATTGAAGGGGAATCTGGCAAAGGCAAGTCCACTCTGCTGCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          submitted (04-JUL-2002) Takao Isogai, FLJ Project(HRI Team); 2-6-7 Razusa-Kamatari, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@fri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 (bases 1 to 3355)
Isogai,T. and Yamamoto,J.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ninomiya,K., Wagatsuma,M., Kanda,K., Kondo,H., Yokoi,T., Kodaira,H., Furuya,T., Takahashi,M., Kikkawa,E., Omura,Y., At Kodaira,H., Katsuta,N., Sato,K., Tanikawa,M., Yamazaki,M., Sato,K., Tanikawa,T., Vamazaki,M., Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Wakamatsu,A., Ishi Yamamoto,J., Isono,Y., Kawai-Hio,Y., Saito,K., Nishikawa,T., Kimura,K., Yamashita,H., Matsuo,K., Nakamura,Y., Sekine,M., Kimura,K., Yamashita,H., Matsuo,K., Nakamura,Y., Sekine,M., Kikuchi,H., Murakawa,K., Kanehori,K., Takahashi-Fujii,A., Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S., Nagahari,K., Masuho,Y., Nagai,K. and Isogai,T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             oligo capping; fis (full insert sequence).
Homo sapiens CD34+ Cells cDNA to mRNA, clone_lib:D9OST2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          clone: D9OST2003791.
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/cell_type="CD34+ Cells"
/clone_lib="D9OST2"
                                                                                                                                                                                                                                                                                                                                                                                                                    /note="cloning vector: pME18SFL3-mRNA from CD34+ cells
after 9-days ODF induction.-primary culture, CD34+ Cel
726 c 774 g 869 t
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/db_xref="taxon:9606"
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Eutheria;
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Primates;
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Matches:
Conservative:
Mismatches:
Indels:
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highly similar
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861
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FEATURES

Clone distribution: MGC clone distribution information can be fo through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 50 Row: a Column: 10 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF

source

/organism="Homo sapiens" /db_xref="LocusID:58484" Location/Qualifiers

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COMMENT
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AUTHORS
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VERSION
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                                                                                                         Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genom
              Gunaratne, P.H., Garcia, A.M., Lu, X., Yoon, V.S., Kowis, C.R., Lawrence, S.,
                                                                                    Sequencing Center
Center code: BCM-HGSC
                                                                                                                                                                                                      NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                      Submitted (06-JUN-2002) National Institutes of Gene Collection (MGC), Cancer Genomics Office, Institute, 31 Center Drive, Room 11A03, Bethesc
                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens, caspase recruitment domain protein 12, MGC:35330 IMAGE:5179909, mRNA, complete cds. BC031555
BC031555.1 GI:21594975
                                                                                                                                                                                                                                                                                                              Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                              Contact: amg@bcm.tmc.edu
                                                                    Web site: http://www.hgsc.bcm.tmc.edu/cdna/
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S., Gibbs, R.A.
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              Hulyk, S.W., Hale, Martin, R.G., Muzn
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National Cancer
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            ThrGluAspSerAlaGlnAlaLeuIleArgGluValLeuIleLysGluLeuAlaGluGly 160
                                                                                                                                                                        CAGAGGGTTCTTTTCCTTCTTGATGGCTACAATGAATTCAAGCCCCCAGAACTGCCCAGAA
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                                                                                                                                                    ATCGAAGCCCTGATAAAGGAAAACCACCGCTTCAAGAACATGGTCATCGTCACCACTACC
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KNWRLTDTEIRILGAFFGKNPLKNFQQLNLAGNRVSSDGWLAFWGVFENLKQLVFFDF
STKEFLPDPALVRKLSQVLSKLTFLQEARLVGWQFDDDDLSVITGAFKLVTA"
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VTTTECLTHIROFGALTAEVGDMTEDSAQALIREVLIKELAEGLLLQIQKSRCLRNL
MKTPLEVVITCAIQMGESEFHSHTGYTLFHTFYDLLIQKKHKHKGVAASDETRSLDH
CGDLALGGVFSHKFDFELQDVSSVNEDVLLTTGLLCKYTAQRFKPKYKFFHKSFOEYT
AGRRLSSLLTSHEPEEVTKGNGYLQKWYSISDITSYSSLLRYTGGSSVEATRAVMKH
LAAVVOHGCLLGLSIAKRFLWROESLQSVKNTDTSTYSSLLRYTGGSSVEATRAVMKH
LAAVOHGCLLGLSIAKRFLWROESLQSVKNTDTSTEDEILKAININSFVECGIHLYOEST
SKSALSOEFEAFFQGKSLYINSGNIPDYLFDFFEHLPNCASALDFIKLDFYGGAMASW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    *Translation="mmfikdnsraliqrmgmtvikqitddlfvwnvlnreevniicce kveqdbargiihmilkkgseschlftksikewnylfeqdlidla odlkdlyhtgsflhyytelddliifmlksfffepvlmrkddhhhrvegltlncllda odlkdlyhtgsflhyktgbidiifmlksffffepvlmrkddhhhrvegltlncllda lospciiegesgkgkstllqriamlwgsgkckaltkfkfvfflrlsraqgglfetlcd
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/clone_lib="NHH_MGC_115"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"
232 . 3306
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THLSDIGEGMDYIVKSLSSEPCDLEEIQLVSCCLSANAVKILAQNLHNLVKLSILDLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EKAAEDTGGIHMEEAPETYIPSRAVSLFFNWKQEFRTLEVTLRDFSKLNKQDIRYLGK
IFSSATSLRLQIKRCAGVAGSLSLVLSTCKNIYSLMVEASPLTIEDERHITSVTNLKT
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/db_xref="GI:21594976"
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CGCATTGCCATGCTCTGGGGCTCCGGAAAGTGCAAGGCTCTGACCAAGTTCAAATTCGTC
                                                                                     ArgIleAlaMetLeuTrpGlySerGlyLysCysLysAlaLeuThrLysPheLysPheVal 40
                                                                                                                                            CTTCAGAGCCCCTGCATCATTGAAGGGGAATCTGGCAAAGGCAAGTCCACTCTGCTGCAG
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ryota; Metazoa; Chordata;
'`~ Entheria; Primates;
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/db_xref="taxon:9606"
277. .3351
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KNWRLTDTEIRLGAFFGKNDLKNEQQLNLAGNRVSSDGWLAFWGVFENLKQLVFFDF
STKEFLPDPALVRKLSGVLSKLTFLGEARLVGWQFDDDDLSVITGAFKLVTA"
1737 c 793 g 874 t
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LSIHDLQNQRLPGGLTDSLGNLKNLTKLIMDNIKMNEEDAIKLAEGLKNLKKMCLFHL
THLSDIGEGMDYIVKSLSSEPCDLEEIQLVSCCLSANAVKILAQNLHNLVKLSILDLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WTTTTECLRHIROFGALTAEVGDMTEDSAQALIREVLIKELAEGLLLQIOKSRCLRNL
MKTPLEVITCA 10MCSSEFHSHTQTTLFHTFYDLLIOKKHKHKGVAASDFIRSLDH
RGDLALEGVFSHKFDDELQDVSSVNEDVLLTGFLCKKTAQREKFKYKYEFHKSFOEVT
AGRRLSSLLTSHEPEEVTKGNGYLQKMVSISDITSTYSSLLRYTCGSSVEATRAVMKH
LAAVVCHGCLLGLSIAKRPLMRQESLOSVKNTTEQEILKAINSFVEEGIHLYQEST
SKSALSQEFEAFFOGKSLYINGGNIEDVLFDFFEHLDWGASALDFIKLDFYGGAMASE
EKAALSQEFEAFFOGKSLYINGGNIEDVLFDFFEHLDWGASALDFIKLDFKLNKQDIRYLGK
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QDLKDLYHTPSFLHEVPLGLFLKSLKSTFFPEILMRKDGHFLKSLQA
LOSFOLIEGESGKGKSTLLQRIAMNGSGKCKFLTEVFFLRLSRAGGLFETLG
QLLDIFGTIRKQTFMAMLLKLRQRVLFLLDGYNEFKPQNCPEIEALIKENHRFKNMVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="CAD19340.1"
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/translation="MNFIKDNSRALIQRMGMTVIKQITDDLFVWNVLNREEVNIICCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mammalia; Eutheria; Primates; Catarrh
1 (bases 1 to 3396)
Damiano,J.S., Stehlik,C., Pio,F., God.
Clan, a novel human ced-4-like gene
Genomics 75 (1-3), 77-83 (2001)
21365712
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AY027787 GI:14324112
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Jolla, CA
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                                                                                                                                                                                                                                                   /gene='
                                                                                                                                                                                                               /note≔"alternatively
                                                                                                                                                                                                                             /gene="CLAN1"
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1. .3396
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1 (bases 1 to 3581)
Gingras,M.-C., Qiu,J. and Margolin,J.F.
Differential expression of the caspase recruitment domain protein
                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                            Homo sapiens
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SKSALSQEFEAFFQGKSLYINSGNIDDYLFDFFELLPKQASALDFIKLDFYGGAMASW
EKAABDTGGIHLMEEADEFYIDSRAVSLFFINWGGEFRTLEVULABFSKLINGDIRYLGK
IFSSATSLRLQIKCAGVAGSLSLVLSTCKNIYSLMVEASPLTIEDERHITSVTNLKT
LSIHDLQNQRLFGGLTDSLGNLKNLTKLIMDNIKMIEDDAIKLAEGLKNLKKWCLFHL
THLSDLGGEMDYIVKSLSSEPCDLEEFIOLVSCCLSANAVKILAQNLHHLYKLSILDLS
ENYLEKDGNEALHELIDRMNVLEQLTALMLPWGCDVQGSLSSLLKHLEEVPQLVKLGL
KNWRLTDTEIRILGAFFGKNPLKNFQDLNLAGNRVSSDGWLAFWGVFENLKQLVFFDF
STKEFLPDFALVRKLSVULSKLTFLOGARLVGWQFDDDDLSVITGAFKLVTA"

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Primates;
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                                                                                                           PhePheLeuArgLeuSerArgAlaGlnGlyGlyLeuPheGluThrLeuCysAspGlnLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (03-MAY-2001) Pediatric/Texas Children's Cancer Center, Baylor College of Medicine, 6621 Fannin St. MC3-3320, Houston, TX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 (bases 1 to 3581)
Gingras,M.-C., Qiu,J. and Margolin,J.F.
Direct Submission
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781 c 843 g 924 t
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ENYLEKDGNEALHELIDRMNVLEQLTALMLPWGCDVQGSLSSLLKHLEEVPQLVKLGL
KNWRLTDTEIRILGAFFGKNPLKNFQQLNLAGNRVSSDGWLAFWGVFENLKQLVFFDF
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EKAAEDTGGIHMEEAPETYIPSRAVSLFFNWKQEFRTLEVTLRDFSKLNKQDIRYLGK
IFSSATSLRLQIKRCAGVAGSLSLVLSTCKNIYSLMVEASPLTIEDERHITSVTNLKT
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CGAATTGCCATGCTCTGGGGCTCCGGAAAGTGCAAGGCTCTGACCAAGTTCAAATTCGTC
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Submitted (18-APR-2002) Genoscope
BP 191 91006 EVRY cedex - FRANCE (E
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1 (bases 1 to 138909)
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n Mar 6, 2000 this sequence version replaced g1:6002386
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/db_xref="taxon:9606"
/chromosome="2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAGAGGGTTCTTTTCCTTGATGGCTACAATGAATTCAAGCCCCAGAACTGCCCAGAA 74792
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                                                                                                                                                                              Sequencing vector: plasmid; 41% Chemistry: Dye-primer ET; 47% of reads Chemistry: Dye-terminator Big Dye; 53% of Assembly program: Phrap; version 0.990319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HTG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo
              Insert size: 147000; agarose-fp
Insert size: 159583; sum-of-contigs
Quality coverage: 6.64 in Q20 bases; agarose-fp
Quality coverage: 6.38 in Q20 bases; sum-of-contigs
                                                                                                          Consensus quality: bases at least Q40 Consensus quality: bases at least Q30 Consensus quality: bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; 1 (bases 1 to 160583)
                                                                                                                                                                                                                                                                          Center: Washington University Genome Sequencing Center Center code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (28-SEP-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo
                                                                                                                                                                                                                                                                                                                                                                           Web site:http://genome.wustl.edu/gsc/index.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequence of Homo sapiens clone
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOTE: This is a 'working draft' sequence. It currently consists of 11 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    as soon as it is available and the accession number will be preserved.
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/db_xref="taxon:9606"
/chromosome="2"
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1. .160583
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (21-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Aug 21, 2002 this sequence version replaced gi:17060568. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
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Submitted (23-NOV-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
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Consensus quality: 173992 bases at least Q40
Consensus quality: 17954 bases at least Q20
Consensus quality: 180012 bases at least Q20
Consensus quality: 180012 bases at least Q20
Insert size: 168000; agarose-fp
Insert size: 181269; sum-of-contigs
Quality coverage: 7.1 in Q20 bases; sum-of-contig
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number wil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NOTE: This is a 'working draft' sequence. It currently consists of 43 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                be preserved.
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                                                                                                                           61 160: gap of 100 bp
161 824: contig of 664 bp in length
825 924: gap of 100 bp
925 1843: contig of 919 bp in length
1844 1943: gap of 100 bp
1944 1945: gap of 100 bp
2616 2715: gap of 100 bp
3318: contig of 603 bp in length
3318: contig of 603 bp in length
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   4624: gap
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                                                                                  yap of 100 bp
318: contig of 603 bp in length
gap of 100 bp
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                       contig of 1106 bp in length of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                           contig of 60 bp in length
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of 861 b
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18392 19794: contig of 1403 bp in length
18795 19894: gap of 100 bp
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11659: contig of 1765 bp in length
1660 21759: gap of 100 bp
1760 23729: contig of 1970 bp in length
1730 23829: gap of 100 bp
1830 25103: contig of 1274 bp in length
1840 25203: gap of 100 bp
1850 2730: contig of 1274 bp in length
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1852 2730: gap of 100 bp
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42 9041: gap of 100 bp
42 9922: contig of 881 bp in length
23 10022: gap of 100 bp
23 11459: contig of 1437 bp in length
60 11559: gap of 100 bp
60 11240: contig of 481 bp in length
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15353: contig of 957 bp in length
15453: gap of 100 bp
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16620: gap of 100 bp
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4187: contig of 3162 bp in 1.
11957: gap of 3777 bp in 1.
45734: contig of 3777 bp in 1.
15834: gap of 100 bp
50885: contig of 4751 bp in 1.
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89239: contig of 9642 bp in length

3339: gap of 100 bp

100740: contig of 11401 bp in lengti
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185469: cont
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13305: contig of 1165 bp in length
105: gap of 100 bp
14296: contig of 891 bp in length
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Homo sapiens psiNAIP mRNA for protein, partial cds. AB048534
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/organism="Mus musculus"
/organism="Taxon:10090"
/db_xref="rtaxon:10090"
/clone="RP24-178L2"
/clone=lib="RPCI-24 Male Mouse
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5586. .6384
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Xu,M., Okada,T., Sakai,H., Miyamoto,N., Yanagisawa,Y., MacKenzle,A.E., Hadano,S. and Ikeda,J.E. Functional human NAIP promoter transcription regulatory elements for the NAIP and Ps.NAIP genes Biochim. Biophys. Acta 1574 (1), 35-50 (2002) 21952357
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Location/Qualifiers
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MacKenzie,A.E., Hadano,S. and Ikeda,J.
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SKFTAQRILPEYRFILSPAFQEFLAGMRLIELIDSDRQEHQDLGILYHIKQETINSPMMTVS
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RGLMQICPQAYFSMVSEHLIYILALKTAYQSNTVAACSPFYLQFLQGRTLITLGALNIQY
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RFQLYFYLSLSSTRPDEGLASIICDQLLEKEGSYTEMCMRNIIQQLKNQYLFLLDDYK
EICSIPQYIGKLIQKNHLSRTCLLIAYRTNRARDIRRYLETILEIKAFPFYNTYCILR
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ERNLAEKEDNVKSYMDMQRRASPDLSTGYWKLSPKQYKIPCLEVDVNDIDVVGQDMLE
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MASAYCNDSIFAYEELRLDSFKDWPRESAVGVAALAKAGLFYTGIKDIVQCFSCGGCL
EKWQEGDDPLDDHTRCFPNCPFLQNMKSSAEVTPDLQSRGELCELLETTSESNLEDSI
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/protein_id="BAB87181.1"
/db_xref="Gi:19909911"
/translation="MPLHIGDFVWDSKVHSLQSSLNIFSLLPTKGRTEHLFFSHILSF
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/chromosome="5"
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Shigehiro, I., Kazuya, M., Harumi, S. and Hitoshi, O.
Excessive ovulation method
Patent: JP 1999113444-A 2 27-APR-1999;
SCIENCE & TECH AGENCY, HARUMI SAKAI
                                                                                                                                                                                                                                                                                                                                                    Strandedness: Double;
                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/db_xref="taxon:9606"
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TTCTACCTCTCCCTTAGTTCCACCAGACCAGACGAGGGGCTGGCCAGTATCATCTGTGAC
                                                                                                                                                                                                                                                                                                                                                                                                             unclassified.
1 (bases 1 to 5502)
Korneluk, R.G., Mackenzie, A.E., Roy, N., USE OF NEURONAL APOPTOSIS INHIBITOR PREATENT: WO 9726331-A 1 24-JUL-1997;
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Sequence 1 from Patent W09726331.
A64509 GI:3717908
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Command line parameters:

-MODEL-frame+_p2n.model -DEV=xlh
-O-/cgn2_1/USPTO_spool_VG09697089/runat_29012003_092753_19709/app_query.fasta_1.981
-O-/cgn2_1/USPTO_spool_VG09697089/runat_29012003_092753_19709/app_query.fasta_1.981
-DB-N_Geneseq_101002 -OFMT-fastap -SUFFIX-p2n.rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE-pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
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-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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| Human APRG polypep | Human NAIP exon 13 | domai | domain | TC DNA C | | CARD-4 | porynuc | | | Himan polynophi | Apoptosis related | | | | CARD-4S | CARD-4S | | DNA of human CARD- | of murin | Mouse CARD-4L (lon | Murine CARD-4L cDN | Nucleotide sequenc | Nucleotide sequenc | Human cDNA #2 enco | Human cDNA #1 enc | Human cDNA encodin | Neuronal apoptosis | Neuronal apoptosis | Ovary cancer relat | Neuronal apoptosis | Human NAIP cDNA. | Human apoptosis in | Gonadotropic hormo | | | Human apoptosis in | Gonadotropic hormo | | Human caspase recr | | | Nucleotide sequenc | Ωı- | | uman cDNA encod | Description |

ALIGNMENTS

ABK22766; 26-MAR-2002 ABK22766 standard; (first cDNA; 891

Caspase recruitment domain; CARD; ss; NB-ARC; ANGIO-R; LRR; SAM; abnormal cell proliferation; cancer; abnormal cell death; apoptosis; autoimmune disease; inflammation; keratinocyte hyperplasia; inflammatory hyperplasia; fibrosis; smooth muscle cell proliferation; balloon angioplasty; restenosis; glioma; carcinoma; sarcoma; melanoma leukæemia; allergy; arthritis; lupus; Schrogen's syndrome; Crohn's disease; graft-versus-host disease; stroke; myocardial infarction; heart failure; neurodegenerative disease; Human cDNA encoding CLAN NACHT.

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Percent Similarity:
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                                                                                                                                                                                                                                                                                                       cc -containing polypeptide, or a CARD, NB-ARC, ANGIO-R, LER OT SAM domain Cf from it, and the polynucleotides encoding them. Also included are a crecombinant vector comprising the polynucleotide, recombinant cells containing the vector (e.g. bacteria, yeast, plant, animal, mammalian cand insect cells) and an anti-CARD antibody. The CARD-containing polypeptide and CARD-encoding nucleic acid are useful for treating a pathology characterised by abnormal cell proliferation (e.g. cancer), cancers, abnormal cell death (apoptosis), autoimmune diseases or inflammation. In capacitation, the polypeptide and nucleic acid are useful for treating a pathology characterised by abnormal cell proliferation. In capacitation, the polypeptide and nucleic acid are useful for treating capacitation cell proliferation in flammatory hyperplasia, fibrosis, smooth capacitation cell proliferation in arteries following balloon angioplasty carcinomas, sarcomas, melanomas, leukaemias, callengies, arthritis, lupus, schrogen's syndrome, Crohn's disease, callergies, arthritis, lupus, schrogen's syndrome, Crohn's disease, cancer disease, or immunodeficiency associated disease or Alzheimer's
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10-OCT-2000;
14-MAR-2001;
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                                                                     PhePheLeuArgLeuSerArgAlaGlnGlyGlyLeuPheGluThrLeuCysAspGlnLeu
                                   ArgIleAlaMetLeuTrpGlySerGlyLysCysLysAlaLeuThrLysPheLysPheVal
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13-MAR-2000;
03-OCT-2000;
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                            Agarwal
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                            Murdoch
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2000US-0188916.
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                                                                                                        The sequence represents a cDNA which encodes the human caspase CC recruitment domain 12 (CARD-12) polypeptide. CARD domains are found in a CR number of proteins that transmit signals that activate apoptosis and CC inflammatory pathways in response to stress and other stimuli. Therefore, CC CARD-12 and its corresponding nucleic acid may be used in treatment and CC diagnosis of patients suffering from disorders associated with an CC abnormal level (an increase or a decrease) of apoptotic cell death or CC abnormal activity of stress-related pathways. The disorders include CC cancer, viral infections (e.g. caused by poxviruses, adenoviruses), CC autoimmune disorders (e.g. Alzheimer's disease, amyotrophic lateral CC selerosis), haematologic diseases (e.g. aplastic anamia, myocardial CC infarction, stroke), inflammatory and immune system disorders (e.g. caused by contact dermatitis, CC control disease, insulin-dependent diabetes, contact dermatitis, CC psoriasis, graft rejection), bacterial infections (e.g. tuberculosis, contact dermatitis, contact dermati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cancer; viral infection; poxvirus; adenovirus; autoimmune disorder; systemic lupus erythematosis; arthritis; neurological disorder; stroke; Alzheimer's disease; amyotrophic lateral sclerosis; haematologic disease; aplastic anaemia, myocardial infarction; inflammatory disorder; Crohn's disease; insulin-dependent diabetes; contact dermatitis; psoriasis; graft rejection; bacterial infection; lepromatous leprosy; tuberculosis; ischaemic brain injury; hypoxic brain injury; ss; kidney ischaemia; reperfusion injury; acute bacterial meningitis; excitotoxic brain damage; liver disease.
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                                                                   Human; secreted polypeptide; nervous disease; muscular disease; tumour; gastrointestinal ulceration; spinal cord disease; trachea disease; thyroid gland disease; ovary disease; prostate disease; heart disease; renal gland disease; small intestine disease; thymus disease; heart disease; lymph node disease; smuscular system disease; colon disease; lymph node disease; muscular system disease; colon disease; lipase deficiency; cystic fibrosis; panoreatitis; clot formation; myocardial infarction; angiopolasty; liver disease; coagulation disorder; miorobial disease; immune disorder; inflammation; transplant rejection; bone thickness; bone density; ferroxidase loss; apoptosis; vascular smooth cell proliferation; vaccine; ss.
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Percent Similarity:
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13-MAR-2000;
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Length:
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10-OCT-2000;
14-MAR-2001;
23-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           abnormal cell proliferation; cancer; abnormal cell death; apoptosis; autoimmune disease; inflammation; keratinocyte hyperplasia; inflammation; pyperplasia; fibrosis; smooth muscle cell proliferation; balloon angioplasty; restenosis; glioma; carcinoma; sarcoma; melanoma; leukaemia; allergy; arthritis; lupus; Schrogen's syndrome; Crohn's disease; graft-versus-host disease; stroke; myocardial infarction; heart failure; neurodegenerative disease; parkinson's disease; Alzheimer's disease; HIV;
                        The invention relates to an isolated caspase recruitment domain (CARD) containing polypeptide, or a CARD, NB-ARC, ANGIO-R, LRR or SAM domain from it, and the polynucleotides encoding them. Also included are a recombinant vector comprising the polynucleotide, recombinant cells containing the vector (e.g. bacterla, yeast, plant, animal, mammalian and insect cells) and an anti-CARD antibody. The CARD-containing polypeptide and CARD-encoding nucleic acid are useful for treating a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1039
                                                                                                                                                                                                                                       Claim 1;
                                                                                                                                                                                                                                                                                           arthritis or stroke
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polypeptide and CARD-encodi
pathology characterised by
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                                                                                                                                                                                                                                                                                                              caspase recruitment domain (CARD)-containing polypeptides and oding nucleic acids, useful for treating abnormal cell proliferation cell death, autoimmune diseases or inflammation, e.g. carcinomas,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ThrGluAspSerAlaGlnAlaLeuIleArgGluValLeuIleLysGluLeuAlaGluGly
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; 2000US-0686347.
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Mismatches:
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tomato; monkey; Human; sheep; pig;

dog; sea

sea urchin; expressed

fruit fly; yeast; hamster; macaque;

sequence tag;

Murine 12-OCT-2001

EST-derived

coding

sequence

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17-JUL-2000;
03-AUG-2000;
15-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                           The present invention provides the protein and coding sequences of novel proteins from a variety of organisms, including human, dog, cat, horse, cow, pig, hamster, monkey, macaque, yeast, bacterla, fruit fly, sea urchin and tomato. These were derived from expressed sequence tags (ESTs) from the organism of interest. They can be used in diagnostics, forensics, gene mapping, identification of mutations, to assess forensics, and for nutritional purposes. The present sequence is a cDNA of the present sequence of the present sequence is a cDNA of the present sequence.
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biodiversity;
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                                                                                  GlnArgValLeuPheLeuLeuAspGlyTyrAsnGluPheLysProGlnAsnCysProGlu
                                                                                                                                        PhePheLeuArgLeuSerArgAlaGlnGlyGlyLeuPheGluThrLeuCysAspGlnLeu
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)B; AAM23595.
                                         CAGAGGGTTCTTTTCCTTGTTGGCTACAATGAATTCAAGCCCCCAGAACTGCCCAGAA
                                                                                                                                                                      CGCATTGCCATGCTCTGGGGCTCCGGAAAGTGCAAGGCTCTGACCAAGTTCAAATTCGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polypeptide for treatment of diseases, es and research use -
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         The sequence represents a genomic DNA which encodes the human caspase recruitment domain 12 (CARD-12) polypeptide. CARD domains are found in a number of proteins that transmit signals that activate apoptosis and inflammatory pathways in response to stress and other stimuli. Therefore, CARD-12 and its corresponding nucleic acid may be used in treatment and diagnosis of patients suffering from disorders associated with an abnormal level (an increase or a decrease) of apoptotic cell death or abnormal activity of stress-related pathways. The disorders include cancer, viral infections (e.g. caused by poxviruses, adenoviruses),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Caspase recruitment domain; CARD-12; apoptosis; stress related pathway; cancer; viral infection; poxvirus; adenovirus; autoimmune disorder; systemic lupus erythematosis; arthritis; neurological disorder; stroke; Alzheimer's disease; amyotrophic lateral sclerosis; haematologic disease; aplastic anaemia; myocardial infarction; inflammatory disorder; Crohn's disease; insulin-dependent diabetes; contact dermatitis; psoriasis; graft rejection; bacterial infection; lepromatous leprosy; tuberculosis; ischaemic brain injury; hypoxic brain injury; ds; kidney ischaemia; reperfusion injury; acute bacterial meningitis; excitotoxic brain damage; liver disease.
                                                                                                                                                                                                   Isolated caspase recruitment domain-12 polypeptide and nucleic acids encoding them, useful for treating and diagnosing disorders associated with abnormal apoptosis such as cancer, arthritis and Alzheimer's disease -
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P-PSDB; AAU02881.
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                     cytostatic; cardiant; vasotropic; cerebroprotective; nootropic
neuroprotective; antibacterial; virucide; fungicide; opthalmal
vulnerary; secreted protein; rheumatoid arthritis;
hyperproliferative disorder; cardiovascular disorder; cardiac
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16-MAR-2000;
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18-APR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      system disorder; Alzheimer's disease; infection; ocular infection; wound healing; epithelial cell proliferation; eing; food additive; preservative; antiproliferative.
  2000US-0184664

2000US-0189350

2000US-0189874

2000US-0199076

2000US-0199123

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2000US-0241786.
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2000US-0246610.
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The invention relates to isolated nucleic acid molecules and their CC encoded secreted proteins. The nucleic acids and proteins are used to grevent, treat or ameliorate a medical condition in e.g. humans, mice, CC rabbits, goats, horses, cats, dogs, chickens or sheep. They cC rabbits, goats, horses, cats, dogs, chickens or sheep. They cC to a pathological condition. Antibodies to the proteins can also be used in alleviating symptoms associated with the disorders and in cC immunosorbant assays (ELISA). Disorders which are disposed or treated include autoimmune diseases e.g. radioimmunoassays or enzyme linked cc include autoimmune diseases e.g. rheumatoid arthritis, created include autoimmune diseases e.g. neoplasms of the breast or liver, cc cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders (c.g., cerebral ischaemia, angiogenesis, nervous system disorders e.g. cardiovascular disorders e.g. cardiac arrest, viruses and fungical occupant of sorders e.g. corneal infection, and many other clisred in the specification. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sumburn, to maintain organs before crease atood additive or preservative to increase or decrease storage can also the content of primary tissues.
capabilities, fat content, lipid, protein, carbohydrate, vitamins minerals, cofactors and other nutritional components. The present sequence encodes a novel secreted protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-DEC-2000;
05-JAN-2001;
                                            capabilities,
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DB; AAU16588.
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d additives or preservatives
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                                               vitamins,
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δ 밁 Ωy 뫄 δÃ 밁 δÃ 밁 δÃ US-09-697-089-2_COPY_161_323 (1-163) Percent Similarity:
Best Local Similarity:
Query Match: Score: Alignment No 481 306 366 246 426 40 08 60 21 LeuGlnSerProCysIleIleGluGlyGluSerGlyLysGlyLysSerThrLeuLeuGln ArgGlnArgValLeuPheLeuLeu ArgIleAlaMetLeuTrpGlySerGlyLysCysLysAlaLeuThrLysPheLys-PheVa CTTCAGAGCCCCTGCATCAATGAAGGGGAATCTGGCAAAGGCAAGTCCAYTCTGCTGCAG CGGCAGAGGGTTCTTTCNTCTTG CTTCTTTCCTCCTGTTCAGCAGGGCCCAGGGTGGGACTTTTTGAAACCCTCTGTGATCAA lPhe-PheLeuArgLeuSerArgAlaGlnGly-GlyLeuPheGluThrLeuCysAspGln |||| ||||||| CGCATTGCCATGCTCTGGGGCTCCGGAAAGTGCAAGGCTCTGACCAAGTTTCAANTTCGT Scores: TTCCG-GGTATACCGGGACA-TTCAGGAGGCAGACATTCAGGCCNGGT---GCTGAGGTG 6.88e-27 276.00 81.11% 76.67% 33.29% 504 87 × Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: AAS26575 (1-522) 522 69 13 13

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RESULT 9 AAX58001

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                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence encodes a gonadotropic hormone. The invention relates to an excessive ovulation animal, which is a transgenic animal with a totipotent cell containing a DNA fragment containing a promoter sequence and a gonadotropic hormone coding sequence. The DNA fragment is in the somatic cell chromosome. The excessive ovulation animal is useful for improving the productivity animals. The method can improve the productivity of a useful animal.
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totipotent cell; soma:
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                                     LeuArgGlnArgValLeuPheLeuLeuAspGlyTyrAsnGluPhe---
                                                                                                GlnLeuLeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLys
                                                                                                                                                PhePheLeuArgLeuSer----ArgAlaGlnGlyGlyLeuPheGluThrLeuCysAsp 58
                                                                                                                                                                           AAAATAGCTTTTCTGTGGGCATCTGGATGCTGTCCCCCTGTTAAACAGGTTCCAGCTGGTT
                                                                                                                                                                                         ArgIleAlaMetLeuTrpGlySerGlyLysCysLysAlaLeuThrLysPheLysPheVal
                                                                                                                                                                                                                                                  LeuGlnSerProCysIleIleGluGlyGluSerGlyLysGlyLysSerThrLeuLeuGln
AsnCysProGluIleGluAlaLeuIleLysGluAsnHisArgPheLysAsnMetValIle 116
                       TTAAAGAATCAGGTCTTATTCCTTTTAGATGACTACAAAGAAATATGTTCAATCCCTCAA
                                                                         CAGCTCCTAGAGAAAGAAGGATCTGTTACTGAAATGTGCATGAGGAACATTATCCAGCAG
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DB; AAY14080.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Page 9-11; 18pp; Japanese
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39.55%
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Conservative:
Mismatches:
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Best Local Similarity:
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P-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence encodes a human apoptosis inhibitory protein. The apoptosis inhibitory protein is useful for the elucidation of the mechanism of various apoptosis diseases such as human spinal muscular atrophy and the diagnosis, the prevention and the treatments of the prevention and the treatments of the prevention and the treatments of the prevention and the treatments of the prevention and the treatments of the prevention and the treatments of the prevention and the treatments of the prevention and the treatments of the prevention and the treatments of the prevention and the treatments of the prevention and the treatments of the prevention and the treatments of the prevention and the treatments of the prevention and the treatments of the prevention and the treatments of the prevention and the treatments of the prevention and the treatments of the prevention and the prevention and the prevention and the prevention and the prevention and the prevention and the prevention and the prevention and the prevention and the prevention and the prevention and the prevention and the prevention and the prevention and the prevention and the prevention and the prevention and the prevention and the prevention and the prevention and the prevention and the prevention and the prevention and the prevention and the prevention and the prevention and the prevention and the prevention and the prevention and the prevention and the prevention and the prevention and the prevention and the prevention and the prevention and the prevention and the prevention and the prevention and the prevention and the prevention and the prevention and the prevention and the prevention and the prevention and the prevention and the prevention and the prevention and the prevention and the prevention and the prevention and the prevention and the prevention and the prevention and the prevention and the prevention and the prevention and the prevention and the prevention and the prevention and the prevention and the prevention and the prevention and the p
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 8; Page 13-15; 16pp; Japanese
                                                                                                                                                                                                                                                             1675 TTGAACTCTGTCATGTGTGTGGAGGGTGAAGCTGGAAGTGGAAAGACGGTCCTTCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New apoptosis inhibitory protein - useful for determining mechanism of various apoptotic diseases e.g. human spinal muscular atrophy
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                                          59
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                                                                                                                                                                                                CAGCTCCTAGAGAAAGAAGGATCTGTTACTGAAATGTGCATGAGGAACATTATCCAGCAG
                      GlnLeuLeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLys 78
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DB; AAY09540.
                                                                                   TTCTACCTCTCCCTTAGTTCCACCAGACCAGACGAGGGGGCTGGCCAGTATCATCTGTGAC
                                                                                                                            PhePheLeuArgLeuSer----ArgAlaGlnGlyGlyLeuPheGluThrLeuCysAsp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               б
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RESULT 11
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XX Ney
I 19-
PR 19-
PR 19-
PR 19-
PR 19-
PR 119-
P
This sequence represents the cDNA sequence for the human neuronal CC apoptosis inhibitor protein (NAIP). This sequence was found on a region CC of the human chromosome 5q13. This sequence was isolated from a yeast CC artificial chromosome (YAC) contig containing the D5x435-D5x112 interval CC from the chromosome 5q13. Mutations in this gene, are causative of spinal CC muscular atrophy (SMA) types I, II, and III. SMAs are a group of CC autosomal recessive, neurodegenerative disorders. SMAs are classified CC into the three types based upon the age of onset (with type I being the CC severest form with the earliest age of onset). All three types are CC characterised by the degeneration of the alpha motor neurons of the Spinal cord manifesting as weakness and wasting of the proximal voluntary CC muscles. The most common mutations of this sequence are thought to be CC deletions of exons 5 and 6, and reductions in the copy number of the CC gene. This gene, (and primers and probes based on this gene) can be used CC for the diagnosis of SMA, and for directing the formulation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Š
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 4; Page 64-67; 113pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ikeda J,
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18-OCT-1994;
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DB; AAR89217.
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Roy N;
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V OTTAWA.
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94GB-0021019
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= a
/product= neuronal apoptosis inhibiting protein
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showing homology value of the can be used
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                                                                                                                                                                                                                                                                                                                                                      gene therapy; cancer; AIDS;
spinal muscular atrophy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAT71263;
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                          Korneluk RG,
                                                                                                                     19-JAN-1996;
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                                                                                                                                                                                                                24-JUL-1997
                                                                                                                                                                                                                                                              WO9726331-A2
                                                                                                                                                                                                                                                                                                                                                                                                     Neuronal apoptosis inhibitor protein; NAIP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neuronal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-OCT-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   apoptosis
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                                                                         OTTAWA.
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                          Mackenzie
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1558
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                          ΑE,
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                          Robertson
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Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A new neuronal apoptosis inhibitor protein (NAIP) cDNA clone (AAT71263) was isolated from a human foetal spinal cord cDNA library by probing with the genomic insert in cosmid 25086, containing a CATT locus. An additional coding sequence (AAT71264), including exon 14a (see also AAT71265 and AAT71266), was subsequently obtd. The NAIP DNA sequence including exon 14a appears to be a predominant gene isoform which is not deleted or mutated in spinal muscular atrophy (SMA) patients. The NAIP gene was mapped to 5q.13.1. NAIP (see also AAW20032 and AAW20033) is a negative regulator of apoptosis, partic. neuronal apoptosis and, when deficient or absent, contributes to neurodegenerative phenotypes such as SMA and amyotrophic lateral sclerosis.
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           Gonadotropic hormone; excessive ovulation totipotent cell; somatic cell chromosome;
                                             Gonadotropic hormone coding sequence
                                                                                             AAX58000;
                                                                                                                 AAX58000 standard;
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                                                                      20-JUL-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     neuronal inhibitor of apoptosis - useful for diagnosing and ating, e.g. cancer, AIDS or amyotrophic lateral sclerosis
                                                                                                                                                                                                                                                                                                  ArgIleAlaMetLeuTrpGlySerGlyLysCysLysAlaLeuThrLysPheLysPheVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Scores:
                                                                                                                                                              ATTGCTGTCCGTACAAACAGGGCCAGGGACATCCGCCGATAC
                                                                                                                                                                                  ValThrThrThrGluCysLeuArgHisIleArgGlnPhe
                                                                                                                                                                                                                                                      TTAAAGAATCAGGTCTTATTCCTTTTAGATGACTACAAAGAAATATGTTCAATCCCTCAA
                                                                                                                                                                                                                                                                                                                         GlnLeuLeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLys
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                                                                     (first
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236.50
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Matches:
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Indels:
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             animal; transgenic animal;
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Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       containing a promoter sequence and a gonadotropic hormone coding sequence. The DNA fragment is in the somatic cell chromosome. The excessive ovulation animal is useful for improving the productivity animals. The method can improve the productivity of a useful animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim
AAX56272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transgenic animal with a totipotent cell containing a DNA fragment containing a PNA fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         An excessive ovulation animal - productivity of animals
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(SAKA/) SAKAI H
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                                                                                                                                                              AsnCysProGluIleGluAlaLeuIleLysGluAsnHisArgPheLysAsnMetValIle 116
                                                                                                                                                                                                                                                                                        CAGCTCCTAGAGAAAGAAGGATCTGTTACTGAAATGTGCATGAGGAACATTATCCAGCAG
                                                                                                                                                                                                                                                                                                                     GlnLeuLeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLys
                                                                                                                                                                                                                                                                                                                                                           TTCTACCTCTCCCTTAGTTCCACCAGACCAGACGAGGGGGCTGGCCAGTATCATCTGTGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                  AAAATAGCTTTTCTGTGGGCATCTGGATGCTGTCCCCTGTTAAACAGGTTCCAGCTGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence encodes a gonadotropic hormone. invention relates to an excessive ovulati
                                                                     ATTGCTGTCCGTACAAACAGGGCCAGGGACATCCGCCGATAC
                                                                                                                                                                                                               TTAAAGAATCAGGTCTTATTCCTTTTAGATGACTACAAAGAAATATGTTCAATCCCTCAA
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standard;
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                                                                                                                                            -GTCATAGGAAAACTGATTCAAAAAAACCACTTATCCCGGACCTGCCTATTG
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 ValThrThrThrGluCysLeuArgHisIleArgGlnPhe
                                           AsnCysProGluIleGluAlaLeuIleLysGluAsnHisArgPheLysAsnMetValIle 116
                                                                     TTAAAGAATCAGGTCTTATTCCTTTTAGATGACTACAAAGAAATATGTTCAATCCCTCAA
                                                                               LeuArgGlnArgValLeuPheLeuLeuAspGlyTyrAsnGluPhe-----
                                                                                                                 CAGCTCCTAGAGAAAGAAGGATCTGTTACTGAAATGTGCATGAGGAACATTATCCAGCAG
                                                                                                                                      GlnLeuLeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLys
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                                                                                                                                                                                       by hybridomas, prepared by fusing antibody-producing cells of mammals immunized with an immunogen containing residues 256-586 or 841-1052 of a 1403 residue amino acid sequence, fully defined in the specification, or their partial sequence, with a myeloma cell line. The monoclonal antibodies are for the study of apoptosis disease onset mechanism, disease diagnosis and development of drugs to prevent and treat apoptosis-related diseases. The quantitation method with the monoclonal antibodies is simple and accurate by using a biological specimen. This sequence encodes the human apoptosis inhibitory protein NAIP which is described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAIP; apoptosis inhibiting protein; monoclonal antibody; diagnosis; apoptosis disease onset mechanism; drugs development; prevention;
                                                                                                                                                                  Sequence 5984
                                                                                                                                                                                                                                                                                                                                 Example 1; Page 31-34; 36pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                       Simple and accurate quantitation of human apoptosis inhibitory protein (NAIP) with monoclonal antibodies, for disease diagnosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2026 ATTGCTGTCCGTACAAACAGGGCCAGGGACATCCGCCGATAC
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Command line parameters:

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-DB-EST -OFMT-fastap -SUFFIX-p2n.rst -MINMATCH-0.1 -LOOPCL-0 -LOOPEXT-0

-UNITS-blts -STARF-1 -END--1 -MAXRIX-blosun62 -FRANS-buman40.cdi -LIST-45

-DOCALIGN-200 -THR_SCORE-pct -THR_MAX-100 -THR_MN0 - ALIGN-15 -MODE-LOCAL

-OUTFMT-pto -NORM-ext -HEAPSIZE-500 -MINLEN-0 -ALIGN-15 -MODE-LOCAL

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-USER-US09697089_8CGN_1_1_1985_8runat_29012003_092754_19729 -NCPU-6 -ICPU-3

-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES-0 -WAIT -LONGLOG -DEV_TIMEOUT=120

-MARN_TIMEOUT=30 -THREADS-1 -XGAPOP=10 -XGAPEXT-7

-YGAPOP-10 -YGAPEXT-0.5 -DELOP-6 -DELEXT-7
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. 44403376544 44103376544 44103376544 622 318 274 272 231.5 226 139.5 133.5 133.5 121.5 123 121.5 123 121.5 123 121.5 123 121.5 123 123.5 12 Score 86 90.5 88.5 93 95.5 94.5 94 Query Match 116.38 116.38 116.38 117.38 11 Length 740 1156 959 870 782 409 1039 523 3368 3368 1098 420 831 682 639 639 DB 8 BE932231 AI344276 BJ228034 BG994836 BW504276 BW504276 BE887277 AZ138405 AA853879 BE1685879 BE731237 BE7468715 BE468715 BE468715 BA397492 BC012789 AZ192862 AZ209193 AL544013 BE374417 AL652549 AZ941653 CNS02NV1 AZ171618 BC021272 IJ AZ362463 AZ762115 BQ365804 BH267158 CH230-19B BH36812 CH230-19E BH358172 CH230-18E BH358172 CH230-18E BH477340 AGENCOURT BH293386 CH230-0466 AZ36246 1 M0017903 AL652549 AL652549 AZ941653 2M0201C01 BG99434 PM0-HT116 BG99434 PM0-HT116 BG99434 PM0-HT16 BG99434 PM0-HT16 BG99437 F015018592 AZ188405 SP_0157_B BA853292 NHTBCae04 B168879 60309957 BE731237 601567129 BA853292 NHTBCae04 B168879 60309957 BE731237 60157129 BA853292 NHTBCae04 B168879 F0130955 BA853292 NHTBCae04 B168879 F0130955 BA853292 NHTBCae04 B168879 F0130955 BA853292 NHTBCae04 B168879 F0130955 BA853292 NHTBCae04 B1688715 IPHdk0035 BG745278 602723479 AZ171618 SP_0120, BC012778 Homo sapi BC012778 Homo sapi BC012778 Homo sapi BC012778 Homo sapi BC012778 Homo sapi BC012778 Homo sapi BC012778 Homo sapi BC012778 Homo sapi BC01278 Homo sapi Description BB627584 BB627584

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| REFERENCE AUTHORS | | ORGANISM | SOURCE | KEYWORDS | VERSION | ACCESSION | | DEFINITION | LOCUS | BB627584 | RESULT 1 |
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| <pre>1 (bases 1 to 650) Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., , Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda</pre> | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. | Mus musculus | house mouse. | EST. | BB627584.1 GI:16465218 | BB627584 | musculus cDNA clone 9530011P19 5', mRNA sequence. | BB627584 RIKEN full-length enriched, adult male urinary bladder Mus | BB627584 650 bp mRNA linear EST 26-OCT-2001 | | |

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URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. . 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
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Please visit our web site (http://genome.gsc.riken.go.jp) for further details.

e mouse tissues.
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The Institute of Physical and Chemical Research (RIKEN)
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Konno, H., Fikunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sug
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Project of Genome Exploration Research Group in Riken
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                                                                                    Jong,P. and Fraser,C.M.
Rat BAC End Sequences from
Unpublished (1999)
Other_GSSs: CH230-19B22.TV
Contact: Shaying Zhao
Contact: Shaying Zhao
                                                  Department of Eukaryotic Genomics
The Institute for Genomic Researc
9712 Medical Center Dr., Rockvill
                                                                                                                                                                      1 (bases 1 to 619) Zhao, S., Shetty, J.,
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Rattus norvegicus
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szhao@tigr.org
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                                                                                                                         Rattus norvegicus
Eukaryota; Metazoa;
Mammalia; Eutheria;
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BH348412
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Unpublished Other_GSSs:
                                                         Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., Geer,K., Shvartsbeyn,A., Gebregeorgis,E., Overton,L., Russell,D., Chen,D., Riggs,F.,
                             Rat BAC End
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/strain="BN/SsNHsd/MCW"
/db_xref="taxon:10116"
/clone="CH230-19B22"
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38.36%
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Rodentia;
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Conservative:
Mismatches:
Indels:
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Sciurognathi; Muridae; Murinae;
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ng (pdejong@mail.cho.org).
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Best Local Similarity:
Query Match:
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CH230-18E7.TJB CHORI-230 Segment 1
CH230-18E7, DNA sequence.
BH358172
BH358172.1 GI:17288906
 zhao, S., Shetty, J., Sl, A., Gebregeorgis, E.,
                                                            Rattus norvegicus
Eukaryota; Metazoa;
Mammalia; Eutheria;
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page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.
plate: 42 row: F column: 7
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Clones are derived from the rat BAC library Cl
(http://www.chori.org/bacpac/rat230.htm). For
availability, please contact Pieter de Jong ([
Clones may be purchased from BACPAC Resources
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Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
                                               Rattus
                                                                                                          Norway rat
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                              (bases 1 to 817)
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/note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: E
CHORI-230 Rat (BN/SSNHSd/MCW) BAC library produced
Pieter de Jong"
124 c 146 g 115 t
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/strain="BN/SsNHsd/MCW"
/db_xref="taxon:10116"
/clone="CH230-42F7"
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/sex="Female"
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Rodentia;
Shatsman,S., Tsegaye,G., Geer,K., Shvartsbeyn
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BM477340.1
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ageNCOURT_6485124 NIH_MGC_85
5', mRNA sequence.
BM477340
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Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/or ering_information.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
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Rat BAC
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Other_GSSs: CH230-18E7.TVB
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Class: BAC ends.
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301 838 0208
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/note-"Vector: pTARBAC2.1; Site_1: EcoRI;
CHORT-230 Rat (BN/SSNHSd/MCW) BAC library
Pieter de Jong"
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/db_xref="taxon:10116"
/clone="CH230-18E7"
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                                                                     ValThrThrThrGluCysLeuArgHisIleArgGlnPhe 130
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ATTGCTGTCCGTACAAACAGGGCCAGGGACATCCGCCGATAC
                                                                                                                                                                                                                         AsnCysProGluIleGluAlaLeuIleLysGluAsnHisArgPheLysAsnMetValIle 116
                                                                                                                                                                                                                                                                                                       TTAAAGAATCAGGTCTTATTCCTTTTAGATGACTACAAAGAAATATGTTCAATCCCTCAA
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Tissue Procurement: Lou Staudt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1999)
Contact: Robert Strausberg,
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National Institutes of Health, N
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Plate: LLAM12272 row
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/Clone=lib="NIH_MGC_85"
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/Clone=lib="NIH_MGC_85"
/Clone=lib="NIH_MGC_85"
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/Inb_host="DH10B (phage-resistant)"
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/db_xref="taxon:9606"
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                        130
                                        146 GlnAlaLeuIleArgGluValLeuIleLysGluLeuAlaGluGlyLeuLeu 162
                                                                                                                   126 HisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMetThrGluAspSerAla 145
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                      CGAGTTCTCATCCGGGAAGTGCTGATAAATGAACTGGCTGAAGGCTTGTTG
                                                                                                                                                                           AAGGAAAACCATCG-TTTAAGAACATGGTCATTGTCACCACCACCACGGAGTGCCTGAGG 69
                                                                                                  CACATCAGACACGTTGGCCCCCTGACTGTGGAGGTGGGAGATATGACCGAAGACAGCGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: szhao@ttigr.org
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/or ering_information.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
plate: 44 row: G column: 15
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,A., Gebregeorgis,E., Overton,L., Russell,D., Chen,D., Riggs,F., de
Jong,P. and Fraser,C.M.
Rat BAC End Sequences from Library CHORI-230 EcoRI segment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BH293386 697 bp DNA linear GSS 30-NOV-200: CH230-44G15.TV CHORI-230 Segment 1 Rattus norvegicus genomic clone
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The Institute for Genomic Research
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Fax: 301 838 0208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Shaying Zhao
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165 c 190
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CHORI-230 Rat (BN/SSNHSd/MCW) BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /sex="Female"
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Eutheria; Rodentia;
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US-09-697-089-2_COPY_161_323 (1-163) x AZ362463 (1-546)
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                                                                                                                                 Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: d
Plate: 0107 row: N column: 03
Seg primer: CACACAGGAAACAGCTATGACC
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Location/Qualifiers
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Fax: 801 585 7177
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University of Utah
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                                                                                                                                                                                           (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (g114732114 jqb1AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Laboratory Mouse DNA Resource
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/strain="C57BL/6J"
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/clone="UUGC1M0107N03"
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Rodentia;
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AZ762115
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Mammalia; Eutheria;
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Seq primer: CACACAGGAAACAGCTATGACC
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                                                        /lab_host="E. Coli strain XL10-Gold, T1-resistant, /note="Vector: PWD42nv; Purified genomic DNA from N musculus C57BL/6J (male) was obtained from the Jac Laboratory Mouse DNA Resource
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through 0.005 inch orifice at constant velocity. The sheared DNA
                                                                                                                                         /clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
                                                                                                                                                                              /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0556N15"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63 TTCTACCTCTCCCTTAGTTCCATCACACCAGACCAGGGACTGGCCAACATCATCTGTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41 PhePheLeuArgLeuSer-----ArgAlaGlnGlyGlyLeuPheGluThrLeuCysAsp 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 ArgileAlaMetLeuTrpGlySerGlyLysCysLysAlaLeuThrLysPheLysPheVal 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       515 bp mR1
MR2-GN0030-210900-021-b10 GN0030 Homo
BQ365804
                                                                                                                                                                                                                                                                                                                               Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare
                                                                                                          Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 and
                                                                                                                                                                                                                                                         Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                    Simpson, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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EST.
                                           Fax: +55-11-2707001
                                                                    Tel: +55-11-2704922
                                                                                                                                                                            Contact: Simpson A.J.G.
                                                                                                                                                                                                                                         sequence tags
                                                                                                                                                                                                                                                                                                           M.J., Soares, F.,
                                                                                                                                                                                                                                                                                                                                                                                                                        (bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWDA2 (gil47321141gblAF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance. The sheared in the sheared in the sheared in the sheared in the sheared in the coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance.
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l: asimpson@ludwig.org.br
sequence was derived from
                                                                                                                                                                                                                     Natl. Acad. Sci. U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The
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AL652549
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTGAACTCTGTCATGTGTGTGGAGGGTGAAACTGGAAGTGGAAAGACGGTCCTCCTGAAG 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GACCCAGCTCCTAGAG
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                                                                                                                                                                                                                                                       Silurana tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                         AL652549 XGC-gastrula Silurana tropicalis cDNA clone
                                     Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS_SEQUENCE_ID: TGas028114.sp6
                                                                                                                   Contact: Huckle E
Sanger Centre
                                                                                                                                                             Huckle, E., Taylor, R., Ashurst, J.L., Sanger Xenopus tropicalis EST projec Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                  EST
                                                                                                                                                                                                                                                                                                                                                                                       mRNA sequence
AL652549
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Seq_primer: puc 18 forward
                                                                                                    Hinxton,
                                                                                                                                                                                                                                                                                                                                                                     AL652549.1 GI:17663115
                  Sequencing primer: SP6
                                                                                                                                                                                                                                             Xenopodinae; Silurana.
                                                                                                                                                                                                                                                                                                                             western clawed frog.
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                                                                                                                                                                                                                      bases 1 to 728)
sequence is from a Xenopus Gene Collection (XGC) library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Organ: placenta_normal; Vector: puc18; Site_1: Sme / Site_2: SmaI; A mini-library was made by cloning products derived from ORSTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                                                                  Cambridgeshire, CB10 1SA,
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/db_xref="taxon:9606"
/clone_lib="GN0030"
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          Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0201 row: C column: 01
Seq primer: CACAAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 556.
                                                                                                                  Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                               Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                   AZ941653
AZ941653.1 GI:13804322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AZ941653 556 bp DNA linear GSS 26-APR-200201C01R Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0201C01 R, DNA sequence.
                                                                                                                                                                                                                                     Unpublished (2000)
                                                                                                                                                                                                                                                   plasmid inserts
                                                                                                                                                                                                                                                                  Mouse whole genome
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/lab host="Escherichia coli XLI-blue"
/note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDN
was oligo dT primed from Sug of poly A+ RNA from stages
10-13 gastrulae. EcoRI-NotI cut cDNA was then ligated
into pCS107 with EcoRI at the 5' end and NotI at the 3'
end."
Location/Qualifiers
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/db_xref="taxon:8364"
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                                                                                                        GlyAlaLeu-----ThrAlaGluValGlyAspMetThrGluAspSerAlaGlnAlaLeu 148
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  IleArgGluValLeuIleLysGluLeu-----
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/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0201C01"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114|gb|AF129072.1), a copy number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through 0.005 inch orifice at constant very. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence tags
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High quality sequence start: 24
High quality sequence stop: 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fax: +55-11-2707001
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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150201-002-d06&t3=2001-02-15&t4=1)
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                                                                                                                                                                                                                                                                                     /note="Organ: head_neck; Vector: puc18; Site_1: SmaI; Site_2: SmaI, A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="HT1166"
/dev_stage="Adult"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BG994334
BG994334.1
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 586)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Simpson A.J.G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence tags
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM0&t2=PM0-HT1166-
130201-003-c11&t3=2001-02-13&t4=1)
Seq primer: puc 18 forward
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Ludwig Institute for Cancer Ro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shotgun sequencing of the human transcriptome with ORF expressed
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                                                                                                                                                                                                                                                                             /note-"Organ: head_neck; Vector: pucl8; Site_1: SmaI; Site_2: SmaI, A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions." 137 g 147 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="HT1166"
/dev_stage="Adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
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                                            x BG994334 (1-586)
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                                                                                  7 IleGluGlyGluSerGlyLysGlyLysSerThrLeuLeuGlnArgIleAlaMetLeuTrp
                      GlySerGlyLysCysLysAlaLeuThrLysPheLysPheValPhePheLeuArgLeuSer 46
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                                                                   ATCCTGGGTGATGCTGGGGTGGGCAAGTCCATGCTGCTACAGCGGCTGCAGAGCCTCTGG
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Eco RI site shown at the beginning of the sequence.

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

cDNA Library Preparation: M.B. Soares Lab

cDNA Library Arrayed by: M.B. Soares Lab

DNA Sequencing by: M.B. Soares Lab

Clone distribution: MCC clone distribution information

found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AW504276 361 bp mRNA linear EST 02-MAI UI-HF-BNO-alp-g-07-0-UI.rl NIH_MGC_50 Homo sapiens cDNA clone IMAGE: 9080628 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Ungublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 361)
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                                                                                                                                                                                                                                                                                                                                    Constructed from size fractionated cytoplasmic mRNA (3.5-4.4kb). Directionally cloned. Cells provided by Louis M. Staudt, Ph.D. Library preparation by Maria de Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D. " 119 c 104 g 80 t 2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Homo sapiens"
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GCCACGGGCCGGCTAGACGCAGGGGTCAAATTCTTCTTCCACTTTCGCTGCCGCATGTTC 136

| Qy | Qy Db | us-09- | Alignment Pred. No.: Score: Percent Si Best Local Query Matc DB: | FEATURES SOU BASE COU | | JOURN | REFERENCE AUTHORS TITLE | ONGANIS | ACCESSION VERSION KEYWORDS SOURCE | RESULT 15 BE887277 LOCUS DEFINITION | Db | Qy | В | Qy | Db | Qy | Вb | Qy |
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| 7 GlySerGlyLysCysLysAlaLeuThrLysPheLysPheValPhePheLeuArgLeu-Se 46 | 7 IleGluGlyGluSerGlyLysGlyLysSerThrLeuLeuGlnArgIleAlaMetLeuTrp 26 | 7-089-2_COPY_161_323 (1-163) x BE887277 (1-939) | nment Scores: 0.00247 Length: 939 e: 105.50 Matches: 38 ent Similarity: 45.79% Conservative: 11 Local Similarity: 35.51% Mismatches: 43 y Match: 12.73% Indels: 15 Gaps: 3 | NT Ce | Tissue Procurement: ATCC CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. | Unpubl Contac | 1 (bases NIH-MGC h National | Eukary Mammal | BE887277.1 BE887277.1 EST. human. | BE8872 | 9 GACCTGAGCGGTGCCTGACAGCTCCTGCCCC 331 | | 9 | 8 | 7 | 8 AspGlnLeuLeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeu 77 | 7 AGCTGCTTCAAGGAAAGTGACAGGCTGTGTCTGCAGGACCTGCTCTTCAAGCACTACTGC 196 | ArgAlaGlnGlyGlyLeuPheG |
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Search completed: January 31, 2003, 16:18:52 Job time: 1335.94 secs

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Minimum
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-WARN_TIMEOUT-30 -THREADS-1 -XGAPOP-10 -XGAPEXT-0.5 -FGAPOP-6 -FGAPEXT-7
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1: /cgn2_5/ptodata/.

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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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                                                                                                                                                                                                                                                                                                                                                                          /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
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US-09-207-3598-27
US-09-207-3598-9
US-09-207-3598-9
US-09-245-281-25
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Query Match:
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US-08-836-134-1
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APPLICANT: Morenzie, Abex E.
APPLICANT: Korneluk, Robert G.
APPLICANT: Mahadevan, Mani S.
APPLICANT: Morenzie
APPLICANT: Neuronal Michael
APPLICANT: Ikeda, Joh-e
TITLE OF INVENTION: Neuronal Apoptosis Inhibitor Protein, Gene Sequence Patent No. 6020127
TITLE OF INVENTION: Mutations Causative of Spinal Muscular Atrophy
FILE REFERENCE: 3477-112, 033477/139914
CURRENT APPLICATION NUMBER: US/08/836,134A
CURRENT FILING DATE: 1997-06-20
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PatentIn Ver. 2.0
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SEQ ID NO 1
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TITLE OF INVENTION: Mutations Causative of Spinal Muscular Atrophy
FILE REFERENCE: 3477-112, 033477/139914
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CURRENT FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: 08/836,134
PRIOR FILING DATE: 1997-06-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Neuronal Apoptosis Inhibitor Protein,
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ORGANISM: Homo
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Korneluk, Robert G.
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TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 07334/118001
CURRENT APPLICATION NUMBER: US/09/245,281
CURRENT FILING DATE: 1999-02-05
EARLIER APPLICATION NUMBER: US 09/207,359
EARLIER FILING DATE: 1998-12-08
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SOFTWARE: FastSEQ for Windows Version
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                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-207-359B-42
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Patent No. 6469140
GENERAL INFORMATION:
APPLICANT: Bertin, John
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 09/099,041
PRIOR TLING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: US 09/019,942
PRIOR FILING DATE: 1998-02-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/207,359B CURRENT FILING DATE: 1998-12-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF FILE REFERENCE: 07334-112001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 47
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ORGANISM: Mus musculus
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                                                                   LeuLeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLysLeu
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                                  -TACCCGGAGCAGGACCCCGAGGAGGTGTTC---TCCTTCTTGCTGCGCTTT 1085
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Indels:
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Percent Similarity:
Best Local Similarity:
Query Match:
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US-09-099-041A-27
; Sequence 27, Application US/09099041A
; Patent No. 6340576
; Patent No. 6340576
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APPLICANT: Bertin, John
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CURRENT APPLICATION NUMBER: US/09/099,041A

CURRENT FILING DATE: 1998-06-17
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TYPE: DNA
ORGANISM: Homo
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                                                                                                          LysLeuArgGlnArgValLeuPheLeuLeuAspGlyTyrAsnGluPhe------
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                                                                       CGCTTCCCCCACGTGGCCCTCTTCACCTTCGATGGCCTGGACGAGCTGCACTCGGACTTG
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107.00
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                                -LysProGlnAsnCysPro
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CURRENT PHILIAGION NUMBER: US/09/245,281
CURRENT FILING DATE: 1999-02-05
EARLIER APPLICATION NUMBER: US 09/207,359
EARLIER FILING DATE: 1998-12-08
EARLIER APPLICATION NUMBER: US 09/099,041
EARLIER FILING DATE: 1998-06-17
EARLIER FILING DATE: 1998-06-17
EARLIER FILING DATE: 1998-06-17
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; Sequence 27, Appli

; Patent No. 6369196
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US-09-245-281-27
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Best Local Similarity:
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GENERAL INFORMATION:
APPLICANT: Bertin, John
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
FILE REFERENCE: 07334-112001
CURRENT PELLICATION NUMBER: US/09/207,359B
CURRENT FILING DATE: 1998-12-08
PRIOR APPLICATION NUMBER: US 09/099,041
PRIOR FILING DATE: 1998-06-17
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                                                                                                                                                                      Sequence 27, Application Patent No. 6469140
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TITLE OF INVENTION: NOTE: MOLECULES OF TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 07334/118001
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                 Query Match:
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                                                                                                                       US-09-099-041A-9
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GENERAL INFORMATION:
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                                                                                                                                  LENGTH: 2859
TYPE: DNA
ORGANISM: Homo
                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/09,041A CURRENT FILING DATE: 1998-06-17 PRIOR APPLICATION NUMBER: 09/019,942 PRIOR FILING DATE: 1998-02-06
                                                                                                                                                                                                                                                                                        APPLICANT: Bertin, John
TITLE OF INVENTION: NOVEL MOLECULES
TITLE OF INVENTION: PROTEIN FAMILY
FILE REFERENCE: 07334-076001
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PRIOR FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 47
                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 37
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TYPE: DNA
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US-09-245-281-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/245,281
CURRENT FILING DATE: 1999-02-05
EARLIER APPLICATION NUMBER: US 09/207,359
EARLIER FILING DATE: 1998-12-08
EARLIER APPLICATION NUMBER: US 09/099,041
EARLIER FILING DATE: 1998-06-17
EARLIER APPLICATION NUMBER: US 09/019,942
EARLIER FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 44
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TYPE: DNA
ORGANISM: Homo s
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RESULT 11
US-09-099-041A-25
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Sequence 25, Application US/09099041A Patent No. 6340576
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Patent No. 6469140
GENERAL INFORMATION:
APPLICANT: Bertin, John
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ORGANISM: Homo
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Score:
                               TITLE OF INVENTION: NOVEL MOLECULES OF THE C
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 0734/118001
CURRENT APPLICATION NUMBER: US/09/245,281
CURRENT FILING DATE: 1999-02-05
EARLIER APPLICATION NUMBER: US 09/207,359
EARLIER FILING DATE: 1998-12-08
EARLIER FILING DATE: 1998-02-05
EARLIER APPLICATION NUMBER: US 09/099,041
EARLIER APPLICATION NUMBER: US 09/019,942
EARLIER APPLICATION NUMBER: US 09/019,942
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Best Local Similarity:
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PRIOR FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSEQ for Windows Version 4.0
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CURRENT APPLICATION NUMBER: US/09/099,041A
CURRENT FILING DATE: 1998-06-17
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                 NUMBER OF
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TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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LOCATION: (1)...(1470)
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; ORGANISM: Homo
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            Best Local Similarity:
Query Match:
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APPLICANT: Bertin, John
APPLICANT: Bertin, John
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
FILE REFERENCE: 07334-112001
                                                                                                                                                                                                      SEQ ID NO 25
LENGTH: 3080
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                                                                                                                                                                                                                                   SOFTWARE:
                                                                                                                                                                                     TYPE: DNA
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APPLICANT: Bertin, John
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
FILE REFERENCE: 07334-076001
CURRENT APPLICATION NUMBER: US/09/099,041A
CURRENT FILING DATE: 1998-06-17
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                                                              GlySerGlyLysCysLysAlaLeuThrLysPheLysPheValPhePheLeuArgLeuSer 46
                                                                                                                                              CGCTTCCCCCACGTGGCCCTCTTCACCTTCGATGGCCTGGACGAGCTGCACTCGGACTTG 762
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: NOVEL MOLECULES TITLE OF INVENTION: AND USES THEREOFFILE REFERENCE: 07334/118001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EARLIER APPLICATION NUMBER: US 09/019,942
EARLIER FILING DATE: 198-02-06
NUMBER OF SEQ ID NOS: 44
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EARLIER APPLICATION NUMBER: US 09/207,359
EARLIER FILING DATE: 1998-12-08
EARLIER APPLICATION NUMBER: US 09/099,041
EARLIER FILING DATE: 1998-06-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/245, CURRENT FILING DATE: 1999-02-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo
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GACCTGAGCCGCGTGCCTGACAGCTCCTGCCCC
                                                                                                 LysLeuArgGlnArgValLeuPheLeuLeuAspGlyTyrAsnGluPhe----
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Search completed: January 31, 2003, 15:16:41

Job time : 43.8989 secs

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Title:
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No.
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-Q=/C9n2_1/USPTO_spoo1/US09697089/runat_29012003_092755_19800/app_query.fasta_1.981
-DB-published.Applications_NA -QFMT-fastap -SUFFIX-p2n.rnpb -MINMATCH-0.1
-DOPECL-0 -LOOPEXT-0 -UNITS-bits -START=1 = END=-1 -MATRIX-blosum62
-TRANS-human40.cdi -LIST-45 -DOCALIGN-200 -THR_SCORE-pct -THR_MAX=100
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-MAXLEN=200000000 -USER-US09697089_@CGN_1_1_48_@runat_29012003_092755_19800
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-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS-1 -XGAPOP-10 -XGAPEXT-0.5 -FGAPOP-6
-FGAPEXT-7 -YGAPOP-10 -YGAPEXT-0.5 -DELOP-6 -DELEXT-7
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Match Length DB
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: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
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Sequence 179, App
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| US-09-864-921-187 US-10-002-974-53 US-10-002-974-58 US-10-002-974-68 US-10-002-974-68 US-10-002-974-68 US-10-002-974-68 US-10-002-974-88 US-10-002-974-88 US-10-002-974-98 US-10-002-974-98 US-10-002-974-98 US-10-002-974-93 US-10-002-974-93 US-10-104-269-1 US-10-002-974-3 US-10-118-984-42 US-10-118-984-27 US-09-728-721-27 US-09-728-721-27 US-09-728-721-9 US-09-728-721-9 US-10-118-984-9 US-09-728-721-9 US-10-105-931-25 | -09-841-739 -09-841-739 -09-764-841-739 -09-764-873-322- 08-913-322- 08-913-322- 08-913-322- 08-913-323-381 -09-833-381 |
| Sequence 187, App Sequence 53, Appl Sequence 56, Appl Sequence 60, Appl Sequence 62, Appl Sequence 64, Appl Sequence 68, Appl Sequence 68, Appl Sequence 84, Appl Sequence 84, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 23, Appl Sequence 27, Appl | 5 6, p 112, 754, 1 754, 2 184, 2 184, 2 184, 2 173, 173, 173, 173, 173, 173, 173, 173, 173, 173, 173, |

ALIGNMENTS

RESULT 1 US-09-864-921-179

GENERAL INFORMATION: Sequence 179, App Patent No. US200

Application US/09864921 20020176853A1

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APPLICANT: Lee, Sug-Hyung
; APPLICANT: Cliveira, Vasco A.
APPLICANT: Hayashi, Hideki
APPLICANT: Hayashi, Hideki
APPLICANT: Hayashi, Hideki
APPLICANT: Hayashi, Hideki
APPLICANT: Pawlowski, Krzysztof
ITILE OF INVENTION: No. US20020176853A1el Card Domain Containing
ITILE OF INVENTION: Polypeptides, Encoding Nucleic Acids, and Methods of U
FILE REFERENCE: P-1.4 752
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US/09/864,921
CURRENT FILING DATE: 2000-05-24
PRIOR APPLICATION NUMBER: US 09/579,240
PRIOR APPLICATION NUMBER: US 09/579,240
PRIOR APPLICATION NUMBER: US 09/686,347
PRIOR APPLICATION NUMBER: US 09/686,347
PRIOR FILING DATE: 2000-10-10
PRIOR FILING DATE: 2000-10-10
PRIOR FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 195
SOCTWARE: FastSEQ for Windows Version 4.0
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Godzik, Adam
Stehlik, Christian
Damiano, Jason S.
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Percent Similarity:
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Query Match:
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          SEQ ID NO LENGTH:
                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                 Sequence 3, Application US/09841739 Patent No. US20020034784A1
                                           CURRENT APPLICATION NUMBER: US/09/841/739
CURRENT FILING DATE: 2001-08-29
PRIOR APPLICATION NUMBER: US 09/697,089
PRIOR FILING DATE: 2000-10-26
PRIOR APPLICATION NUMBER: US 60/161,822
PRIOR FILING DATE: 1999-10-27
NUMBER OF SEQ ID NOS: 16
                                                                                                                               APPLICANT: Bertin, John
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
FILE REFERENCE: 07334-329001
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ORGANISM: HOMO
FEATURE:
                                  SOFTWARE: FastSEQ for Windows
TYPE: DNA
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GENERAL INFORMATION:
APPLICANT: Bertin, John
TITLE OF INVENTION: NOVEL MOLECULES OF THE CAI
FILE REFERENCE: 07334-329001
CURRENT APPLICATION NUMBER: US/09/841,739
CURRENT FILING DATE: 2001-08-29
PRIOR APPLICATION NUMBER: US 09/697,089
PRIOR APPLICATION NUMBER: US 60/161,822
PRIOR APPLICATION NUMBER: US 60/161,822
; NAME/KEY: CDS
; LOCATION: (36)...(3107)
US-09-841-739-1
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                                                                            SEQ ID NO 1
                                                                                                                                                                                                                  Sequence 1, Application US/09841739
Patent No. US20020034784A1
                                                                                               PRIOR FILING DATE: 1999-10-27
NUMBER OF SEQ ID NOS: 16
                                                                                      SOFTWARE: FastSEQ
                                          TYPE: DNA
ORGANISM: Homo
                                  FEATURE:
                                                                LENGTH: 3133
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APPLICANT: Need, John C.
APPLICANT: Bodzik, Adam
APPLICANT: Godzik, Adam
APPLICANT: Stehlik, Christian
APPLICANT: Stehlik, Christian
APPLICANT: Damiano, Jason S.
APPLICANT: Damiano, Jason S.
APPLICANT: Lee, Sug-Hyung
APPLICANT: Hayashi, Hideki
APPLICANT: Hayashi, Hideki
APPLICANT: Hayashi, Hideki
APPLICANT: Hayashi, Hideki
APPLICANT: Pawlowski, Krzysztof
TITLE OF INVENTION: No. US20020176853A1el Card Domain Containing
TITLE OF INVENTION: Polypeptides, Encoding Nucleic Acids, and Methoritic Privation NUMBER: US/09/864,921
CURRENT APPLICATION NUMBER: US/09/864,921
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 09/579,240
PRIOR TILING DATE: 2000-05-24
PRIOR APPLICATION NUMBER: US 09/686,347
PRIOR APPLICATION NUMBER: US 60/275,980
PRIOR FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 195
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APPLICANT: Bertin, John
TITILE OF INVENTION: NOVEL MOLECULES OF THE C
FILE REFERENCE: 0734-729001
CURRENT APPLICATION NUMBER: US/09/841,739
CURRENT FILING DATE: 2001-08-29
PRIOR APPLICATION NUMBER: US 09/697,089
PRIOR PILING DATE: 2000-10-26
PRIOR APPLICATION NUMBER: US 60/161,822
PRIOR FILING DATE: 1999-10-27
NUMBER OF SEQ 1D NOS 16
SOFTWARE: FastSEQ for Windows Version 4.0
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; LOCATION: (277)...(3348)
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                                          Sequence 4, Application US/09841739
Patent NO. US20020034784A1
GENERAL INFORMATION:
APPLICANT: Bertin, John
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
FILE REFERENCE: 07334-329001
CURRENT APPLICATION NUMBER: US/09/841,739
CURRENT FILING DATE: 2001-08-29
PRIOR APPLICATION NUMBER: US 09/697,089
PRIOR APPLICATION NUMBER: US 60/161,822
PRIOR APPLICATION NUMBER: US 60/161,822
PRIOR FILING DATE: 1999-10-27
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 3615
TYPE: NA
                   TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
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                                                               APPLICANT: BETTLIN, John
ITILE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROFILE REFERENCE: 07334-329001
CURRENT APPLICATION NUMBER: US/09/841,739
CURRENT FILING DATE: 2001-08-29
PRIOR APPLICATION NUMBER: US 09/697,089
PRIOR APPLICATION NUMBER: US 60/161,822
PRIOR APPLICATION NUMBER: US 60/161,822
PRIOR APPLICATION NUMBER: US 60/161,822
PRIOR FILING DATE: 1999-10-27
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 3615
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US-09-841-739-4
                                    ; ORGANISM: HOMO US-09-841-739-12
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                                                            TYPE: DNA
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Best Local Similarity:
                                                                                                                                                                                                                                 Sequence 754, Application US/09764864 Patent No. US20020132753A1 GENERAL INFORMATION:
NAME/AL.
LOCATION: (499)
OTHER INFORMATION: r
NAME/KEY: SITE
NAME/KEY: (505)
                                                                                                                                               SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 754
                                NAME/KEY: SITE
LOCATION: (468)
OTHER INFORMATION: NAME/KEY: SITE
LOCATION: (499)
                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/764,864
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM
NUMBER OF SEQ ID NOS: 1792
                                                                                                                                                                                                       APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PTZ23
                                                                                                          LENGTH: 522
TYPE: DNA
ORGANISM: Homo s
FEATURE:
                                                                               NAME/KEY: SITE
LOCATION: (360)
OTHER INFORMATION:
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                                                  US-09-697-089-2_COPY_161_323 (1-163) x US-08-913-322-1 (1-5504)
                                                                                                                                                                                                                                                        TITLE OF INVENTION: USER OF NEURONAL APOPTOSIS INFITTLE OF INVENTION: (NAIP)
FILE REFERENCE: 07891/013001
CUBRENT APPLICATION NUMBER: US/08/913,322
CURRENT FILING DATE: 1997-09-12
EARLIER APPLICATION NUMBER: PCT/IB97/00142
EARLIER APPLICATION NUMBER: GB 9601108.5
EARLIER APPLICATION NUMBER: 1996-01-19
EARLIER FILING DATE: 1996-01-19
NUMBER: 05-01-19
NUMBER: 05-01-19
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Pred. No.:
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                                                                                                                                                                                           LENGTH: 5504
TYPE: DNA
ORGANISM: Homo
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; ORGANISM: Homo sapiens
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APPLICANT: Korneluk, Robert
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                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/08/913,322 CURRENT FILING DATE: 1997-09-12 EARLIER APPLICATION NUMBER: PCT/IB97/00142 EARLIER FILING DATE: 1997-01-17 EARLIER APPLICATION NUMBER: GB 9601108.5 EARLIER FILING DATE: 1996-01-19 NUMBER OF SEQ ID NOS: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: USER OF NEURONAL APOPTOSIS TITLE OF INVENTION: (NAIP) FILE REFERENCE: 07891/013001
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                                                                                   ArgIleAlaMetLeuTrpGlySerGlyLysCysLysAlaLeuThrLysPheLysPheVal 40
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                              PhePheLeuArgLeuSer-----ArgAlaGlnGlyGlyLeuPheGluThrLeuCysAsp 58
                                                               AAAATAGCTTTTCTGTGGGCATCTGGATGCTGTCCCCTGTTAAACAGGTTCCAGCTGGTT
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TTCTACCTCTCCCTTAGTTCCACCAGACCAGACGAGGGGCTGGCCAGTATCATCTGTGAC
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US-09-967-768A-184

Sequence 184, Application US/09967768A

Patent No. US20020150877A1

GENERAL INFORMATION:
APPLICANT: AUGUSTUS, Meena
TITLE OF INVENTION: Cancer Gene Determination
TITLE OF INVENTION: Sets

FILE REFERENCE: 689290-72
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LENGTH: 6124
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                                                                                                        CAGCTCCTAGAGAAAGAAGGATCTGTTACTGAAATGTGCATGAGGAACATTATCCAGCAG
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                                                                                                                                       GlnLeuLeuAspIleProGlyThrIleArgLySGlnThrPheMetAlaMetLeuLeuLys 78
                                                                                                                                                                                                          PhePheLeuArgLeuSer-----ArgAlaGlnGlyGlyLeuPheGluThrLeuCysAsp
AsnCysProGluIleGluAlaLeuIleLysGluAsnHisArgPheLysAsnMetValIle 116
                                                          LeuArgGlnArgValLeuPheLeuLeuAspGlyTyrAsnGluPhe---
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                                    TTAAAGAATCAGGTCTTATTCCTTTTAGATGACTACAAAGAAATATGTTCAATCCCTCAA
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DB:
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Patent No. US20020137028A1
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APPLICANT: Tamai, Katsu
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APPLICANT: MacKenzie,
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TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                US-09-864-921-173
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Best Local Similarity:
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GENERAL INFORMATION:
APPLICANT: Reed, John C.
APPLICANT: Pio, Frederick F.
APPLICANT: Godzik, Adam
APPLICANT: Stehlik, Christian
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LENGTH: 6228
                                                                                 Sequence 173, Application Patent No. US20020176853A1
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SOFTWARE: FastSEQ for
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US-09-697-089-2_COPY_161_323 (1-163) x US-08-913-322-23 (1-6228)
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Damiano, Jason

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APPLICANT: Diveira, Vasco A.
APPLICANT: Hayashi, Hideki
APPLICANT: Pawlowski, Krzysztof
TITLE OF INVENTION: No. US20020176853A1el Card Domain Containing
TITLE OF INVENTION: No. US20020176853A1el Card Domain Containing
TITLE OF INVENTION: Polypeptides, Encoding Nucleic Acids, and Methods of UFILE REFERENCE: P-LJ 4752
CURRENT EPLICATION NUMBER: US.09/864,921
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US.09/579,240
PRIOR APPLICATION NUMBER: US.09/586,347
PRIOR APPLICATION NUMBER: US.09/686,347
PRIOR APPLICATION NUMBER: US.60/275,980
PRIOR APPLICATION NUMBER: US.60/275,980
PRIOR APPLICATION NUMBER: US.60/275,980
PRIOR FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 195
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 173
LENGTH: 888
US-09-833-381-1214

Sequence 1214, Application US/09833381

; Patent No. US20020132090A1

; GENERAL INFORMATION:
APPLICANT: Robison, Keith E.
TITLE OF INFORMATION: NO. US20020132090A1el Nucleic Acid and Protein Homologs
FILE REFERENCE: 5800-119

CURRENT APPLICATION NUMBER: US/09/833,381

CURRENT FILING DATE: 2001-04-11

PRIOR APPLICATION NUMBER: 09/316,448

PRIOR FILING DATE: 2000-02-29

NUMBER OF SEO ID NOS: 2050

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 1214

LENGTH: 2724
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ORGANISM: Homo sapiens
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                    Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature LOCATION: (1)...(2724)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE:
1324
                                                           1282
                                                                                                                                                                                   1168
                                                                                                                        1222 CGGCAGCTGCAGTGCCAAACCACTCTCTGTGCGGACTCTACTCTTTGAGCACTGC 1281
                                                                                                                                                                                                                                             1108 CTGGTGGTGGGTGAGGCGGCAGTGGCAAGAGCACGCTCCTGCAGCGGCTGCACTTGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                No.:
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                              77
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                                                                                                                                                                                                                                                           CTTGACCACCCTGACCGTGTCCTGTTAACCTTTGATGGCTTTGACGAGTTCAAG 1377
                      LeuLysLeuArgGlnArgValLeuPheLeuLeuAspGlyTyrAsnGluPheLys 94
                                                         TGTTGGCCT---
                                                                                                                                                                                   TGGGCTGCAGGG------CAAGACTTCCAGGAATTTCTCTTTGTCTTCCCATTCAGCTGC 1221
                                                                                        CysAspGlnLeuLeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeu 76
                                                                                                                                                 SerArgAlaGln-----
                                                                                                                                                                                                             TrpGlySerGlyLysCysLysAlaLeuThrLysPheLysPheValPhePheLeuArgLeu 45
                                                                                                                                                                                                                                                                                                                                1.32e-06
120.50
48.98%
33.67%
14.54%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,T,C or
                                                           -----GATGTTGGTCAAGAAGACATCTTCCAGTTACTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a
                                                                                                                                                   -----GlyGlyLeuPheGluThrLeu 56
                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                     Indels:
                                                           1323
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Minimum DB :
Maximum DB :
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-Q-/Cg12_1/USPTO_spool/US09697089/runat_29012003_092754_19749/app_query.fasta_1.981
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-TRANS-human40.cdi -LIST-45 -DOCALIGN=200 -THR_SCORE-pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE-LOCAL -OUTFMT-pto -NORM-ext -HEAPSIZE-500 -MINLEN=0
-MAXKEN=2000000000 -USE=-US09697089_@CGN_1_1_3083_@runat_2901203_092754_19749
-NCPU=6 -ICPU=3 -NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPOEXT=0.5 -FGAPOP=6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Perfect score:
Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Command line parameters:
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Delop 6.0 , I
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APPLICANT: Lee, Sug-Hyung
APPLICANT: Oliveira, Vasco A.
APPLICANT: Hayashi, Hideki
APPLICANT: Pawlowski, Krzysztof
TITLE OF INVENTION: Novel Card Domain Containing
TITLE OF INVENTION: Novel Card Domain Containing
TITLE OF INVENTION: Novel Card Domain Containing
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TUTRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 09/579,240
PRIOR APPLICATION NUMBER: US 09/579,240
PRIOR APPLICATION NUMBER: US 09/686,347
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PRIOR APPLICATION NUMBER: US 60/275,980
PRIOR TILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 179, Application:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Reed, John C.
APPLICANT: Pio, Frederick F.
APPLICANT: Godzik, Adam
APPLICANT: Stehlik, Christian
APPLICANT: Damiano, Jason S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
LENGTH: 891
TYPE: DNA
ORGANISM: Homo s
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39 US-09-897-089-12
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2 US-09-578-917
2 US-09-579-240-17
2 US-09-577-408-3077
2 US-09-577-408-3077
PCT-US-07-28643-3
7 US-09-697-089-3
2 US-09-841-739-3
1 US-10-156-733-1
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Sequence 17, Appl
Sequence 3077, Ap
Sequence 3, Appli
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Sequence 3, Appli
Sequence 1, Appli
Sequence 23, Appl
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Sequence 66, Appl
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Sequence 96, Appl
Sequence 96, Appl
Sequence 96, Appl
Sequence 1319, Ap
Sequence 6, Appli
Sequence 6, Appli
Sequence 1319, Ap
Sequence 1, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 12, Appl
Sequence 910, App
Sequence 911, App
                                                                                                                                                                                                                                                                US-10-029-386-22860/c

Sequence 22860, Application US/10029386

GENERAL INFORMATION:

APPLICANT: Penn, Sharron G.

APPLICANT: Hanzel, David R.

APPLICANT: Hanzel, David R.

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXC.

TITLE OF INVENTION: EXPRESSION ANALYSIS TWO

FILE REFERENCE: AEOMICA-X-2

CURRENT APPLICATION NUMBER: US/10/029,386

CURRENT APPLICATION NUMBER: US/10/029,386

CURRENT APPLICATION NUMBER: US/10/029,386

CURRENT APPLICATION NUMBER: US/10/029,386
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; NAME/KEY: CDS
; LOCATION: (1)...
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Best Local Similarity:
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                                                                                                                                                                               SOFTWARE: Annomax Sequence Listing SEQ ID NO 22860 LENGTH: 1976
FEATURE:
OTHER INFORMATION: NOTHER INFORMATION: EOTHER EOTHER INFORMATION: EOTHER EOTHER EOTHER EOTHER EOTHER EOTHER EOTHER EOTHER EOTHER EOTHER EOTHER EOTHER EOTHER EOTHER EOTHER EOTHER EOTHER EOTHER EOTHER EOTHER EOTHER EOTHER EOTHER EOTHER EOTHER EOTHER EOTHER EOTHER EOTHER EOTHER EOTHER EOTHER EOTHER EOTHER EOTHER EOTHER EOTHER EOTHER EOTHER EOTHER EOTHER EOTHER EOTHER EOTHER EOT
                                                                                                                          TYPE: DNA
ORGANISM: Homo sapiens
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APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SIN
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REFERENCE: AEOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine ve
SEQ ID NO 25135
LENGTH: 2002
TYPE: DNA
ORGANISM: Homo sapiens
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US-10-029-386-25135/c
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Query Match:
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                                                                                                                                                                                                                                Sequence 25135, Application US/10029386 GENERAL INFORMATION:
                                                                                                                                                                                                       APPLICANT: Penn, Sharron G. APPLICANT: Rank, David R.
FEATURE:
OTHER INFORMATION: MAP TO AL121653.1
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.36
OTHER INFORMATION: EST_HUMAN HIT: AV656315.1, EVALUE 0.00e+00
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OTHER INFORMATION:
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NT HIT: gi15296399, EVALUE 0.00e+00
EST_HUMAN HIT: AV656315.1, EVALUE 0.00e+00
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; OTHER INFORMATION:
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US-10-029-386-25135
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Best Local Similarity:
                                                      PRIOR APPLICATION NUMBER: 60/187,107
PRIOR FILING DATE: 2000-03-06
PRIOR APPLICATION NUMBER: 60/236,874
PRIOR APPLICATION NUMBER: 60/188,916
PRIOR FILING DATE: 2000-03-13
PRIOR APPLICATION NUMBER: 60/237,846
PRIOR APPLICATION NUMBER: 60/237,846
PRIOR FILING DATE: 2000-10-03
                                                                                                                                                                        Sequence 22, Application PC/TUS0107143
GENERAL INFORMATION:
APPLICANT: SMITHKLINE BEECHAM CORPORATION
APPLICANT: SMITHKLINE BEECHAM p.l.c.
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GP50016
CURRENT APPLICATION NUMBER: PCT/US01/07143
CURRENT FILING DATE: 2001-03-08
BEET OF APPLICATION NUMBER: 60/187/107
NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ fo:
SEQ ID NO 22
LENGTH: 2215
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Percent Similarity:
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Query Match:
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CURRENT APPLICATION NUMBER: US/10/221,097
CURRENT FILING DATE: 2002-09-06
PRIOR APPLICATION NUMBER: PCT/US01/07143
PRIOR FILING DATE: 2001-03-05
PRIOR APPLICATION NUMBER: 60/187,107
PRIOR APPLICATION NUMBER: 60/236,874
PRIOR APPLICATION NUMBER: 60/236,874
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/236,874
PRIOR APPLICATION NUMBER: 60/236,874
PRIOR APPLICATION NUMBER: 60/237,846
PRIOR APPLICATION NUMBER: 60/237,846
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
NUMBER OF SEQ ID NOS: 52
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PCT-US01-07143-22
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APPLICANT: Murdock, Paul R.
APPLICANT: Mixt, Safia K.
APPLICANT: Smith, Randall F.
APPLICANT: Xiang, Zhaoyel COMPOUNDS
FILE REFERENCE: GP50016
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                                                                                           Sequence 15, Application US/09578789
GENERAL INFORMATION:
APPLICANT: John C. Reed
APPLICANT: Frederick Pio
APPLICANT: Frederick Pio
APPLICANT: Adam Godzik
TITLE OF INVENTION: Novel Card Polypeptides
FILE REFERENCE: P-LJ 4141
CURRENT APPLICATION NUMBER: US/09/578,789
CURRENT FILING DATE: 2000-05-23
NUMBER OF SEQ ID NOS: 75
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 FEATURE:
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ORGANISM: Homo
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SEQ ID NO 15
LENGTH: 2343
TYPE: DNA
ORGANISM: Homo Sapien
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(2340)
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APPLICANT: John C. Reed
APPLICANT: Frederick Pi
APPLICANT: Adam Godzik
                                                                                                                                                                                                                                                                                                                                                                           Sequence 15,
                                                                                                                                                                                               TITLE OF INVENTION: Novel Card-Domain Containing TITLE OF INVENTION: Polypeptides, Encoding Nucle: FILE REFERENCE: P-LJ 4211
CURRENT APPLICATION NUMBER: US/09/579,240
CURRENT FILING DATE: 2000-05-24
RUMBER OF SEQ ID NOS: 79
COUNTEDATO: Traction for Mindel Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counter Counte
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GENERAL INFORMATION:
APPLICANT: John C. Reed
APPLICANT: Frederick Pio
APPLICANT: Adam Godzik
TITLE OF INVENTION: Novel Card Polypeptides
FILE REFERENCE: P-LJ 4141
CURRENT APPLICATION UMBER: US/09/578,789
CURRENT FILING DATE: 2000-05-23
NUMBER OF SEQ ID NOS: 75
                                                                                   Alignment
Pred. No.:
                   Query Match:
                               Percent Similarity:
Best Local Similarity:
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SEQ ID NO 17
LENGTH: 2415
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                                                                                                      Pred. No.:
                                                                                                               Alignment Scores:
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SEQ ID NO 17
SEQTH: 2415
                                                                                                                                                                                                                                                                                                                                           Sequence 17, Application US/09579240 GENERAL INFORMATION:
                                                                                                                                                                                                                               TITLE OF INVENTION: Novel Card-Domain Containing
TITLE OF INVENTION: Polypeptides, Encoding Nucleic Acids, and Methods of Use
FILE REPERENCE: P-LJ 4211
CURRENT APPLICATION NUMBER: US/09/579,240
CURRENT FILING DATE: 2000-05-24
NUMBER OF SEQ ID NOS: 79
NUMBER OF SEQ ID NOS: 79
NUMBER OF SEQ ID NOS: 79
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APPLICANT: Frederick Pio
APPLICANT: Adam Godzik
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TYPE: DNA
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US-09-577-408-3077
; Sequence 3077, Application Us; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Tillinghast, Jol
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                                                                                                                                     US-09-577-408-3077
                                                                                                                                                                                                                           SOFTWARE: pt_GCT_genes Version SEQ ID NO 3077 LENGTH: 3018
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APPLICANT:
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CURRENT FILING DATE: 2000-05-18
NUMBER OF SEQ ID NOS: 8502
                                                                                                                                                                                                                                                                                             APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: NOVEL Nucleic
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 792
                                                                                                                                              NAME/KEY: misc_feature
LOCATION: (682)...(2040)
OTHER INFORMATION: simil-
OTHER INFORMATION: Run w
                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                      ORGANISM: Homo
                                                                                                                                                                                                                  TYPE: DNA
                                                                                                     No.:
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Liu, Chenghua
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Pred. No.:
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                                                                                                                                                                                   SEQ ID NO 3
LENGTH: 3072
TYPE: DNA
ORGANISM: Homo:
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TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
FILE REFERENCE: 07334-136WO1
CURRENT APPLICATION NUMBER: PCT/US00/29643
CURRENT FILING DATE: 2000-10-26
PRIOR APPLICATION NUMBER: US 60/161,822
PRIOR FILING DATE: 1999-10-27
NUMBER OF SEQ ID NOS: 11
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; LENGTH: 3072
; TYPE: DNA
; ORGANISM: Homo s
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APPLICANT: Robison, Keith E.
APPLICANT: Robison, Keith E.
TITLE OF INVENTION: NOVEL MOLECULES OF THE C
TITLE OF INVENTION: PROTEIN FAMILY AND USES
FILE REFERENCE: 07334-136001
CURRENT APPLICATION NUMBER: US/09/697,089
CURRENT FILING DATE: 2000-10-26
PRIOR APPLICATION NUMBER: US 60/161,822
PRIOR FILING DATE: 1999-10-27
PRIOR FILING DATE: 1999-10-27
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US-09-697-089-3
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; LENGTH: 3072
; TYPE: DNA
; ORGANISM: HOMO s
US-09-841-739-3
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Best Local Similarity:
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TITLE OF INVENTION: NOVEL MOLECULES OF THE CA
FILE REFERENCE: 07334-329001
CURRENT APPLICATION NUMBER: US/09/841,739
CURRENT FILING DATE: 2001-08-29
PRIOR APPLICATION NUMBER: US 09/697,089
PRIOR APPLICATION NUMBER: US 09/697,089
PRIOR APPLICATION NUMBER: US 00/161,822
PRIOR FILING DATE: 1999-10-27
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SOFTWARE: FastSEQ for Windows
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US-10-156-733-1

Sequence 1, Application US/10156733

GENERAL INFORMATION:

APPLICANT: Alnemri, Emad S.

TITLE OF INVENTION: IPAC, AN ICE-PROTEASE AC

TITLE OF INVENTION: FACTOR

TITLE OF INVENTION: PACTOR

TITLE OF INVENTION UNDEER: US/10/156,733

CURRENT APPLICATION NUMBER: US/10/156,733

CURRENT APPLICATION DATE: 2002-05-24

NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                                Best Local Similarity:
Query Match:
DB:
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; LOCATION: (1)...(3075)
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ORGANISM: Homo
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ThrGluCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMet
                         ACAGAAGACAGCGCCCAGGCTCTCATCCGAGAAGTGCTGATCAAGGAGCTTGCTGAAGGC
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DB:
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Best Local Similarity:
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; LOCATION: (36)...(3107)
PCT-US00-29643-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Millennium Pharmaceuticals, Inc.
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
FILE REFERENCE: 07334-136W01
CURRENT APPLICATION NUMBER: PCT/US00/29643
CURRENT FILING DATE: 2000-10-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: HOMO:
FEATURE:
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                                             ThrGluCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMet 140
                                                                                      IleGluAlaLeuIleLysGluAsnHisArgPheLysAsnMetValIleValThrThrThr
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Search completed: January 31, 2003, 17:55:31 Job time: 2076.15 secs

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-MODEL-frame+_p2n.model -DEV=x1h
-Q-/cgn2_1/USPTO_Spool_VS9697089/runat_29012003_092755_19775/app_query.fasta_1.981
-Q-/cgn2_1/USPTO_Spool_VS9697089/runat_29012003_092755_19775/app_query.fasta_1.981
-DB-Pending_Patents_NA_New -QFMT-fastap -SUFFIX=P2n.rnpn -MINMATCH=0.1
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-TRAMS-human40.cd1 -LIST=45 -DOCALIGN=20 -THR_SCORE-pct -THR_MX=100
-THR_MIN=0 -ALIGH=N-15 -MODE-LOCAL -OUTENT-pto -NORM-ext -HEAPSIZE-500 -MINLEN=0
-MAXLEN=2000000000 -USER-US09697089_eCGN 1_191_@runat_29012003_092755_19775
-NCPU=6 -ICPU=3 -NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT.-LONGLOG
-DEV_TIMEOUT=10 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq:*

2: /cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq:*

3: /cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq:*

4: /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*

5: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:*

6: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:*

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Copyright (c) 1993 - 2003 Compugen Ltd.
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 PCT - US02 - 21946A - 1

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2, Appli
84, Appl
125, App
656, App
697, App
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ALIGNMENTS

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                                                                                                      Query Match:
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                                                                                                                                                                Pred. No.:
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                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Applicat GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Thomas Jefferson University
APPLICANT: Alnemi, Emad S.
TITLE OF INVENTION: IPAF, AN ICE-PROTEASE ACTIVATING
TITLE OF INVENTION: FACTOR
FILE REFERENCE: 480140.477PC
CURRENT APPLICATION NUMBER: PCT/US02/21946A
                                                                                                                                                                                                                                                                                                                                                          CURRENT FILING DATE:
                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo
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LOCATION: (1)...(3075)
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; SEQ ID NO 14
; LENGTH: 3219
; TYPE: DNA
; ORGANISM: Homo sapiens
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APPLICANT: Thomas Jefferson University
APPLICANT: Alnemi, Emad S.
TITLE OF INVENTION: IPAF, AN ICE-PROTEASE ACT:
TITLE OF INVENTION: FACTOR
FILE REFERENCE: 480140.477PC
CURRENT APPLICATION NUMBER: PCT/US02/21946A
CURRENT FILING DATE: 2002-05-24
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                       ArgIleAlaMetLeuTrpGlySerGlyLysCysLysAlaLeuThrLysPheLysPheVal
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; LENGTH: 3545
; TYPE: DNA
; ORGANISM: Homo s
US-10-276-781-111
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DB:
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Best Local Similarity:
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LENGTH: 3545
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                                                                                                                                                                                                                                                                                                                                             APPLICANT: Tang et al.
TITLE OF INVENTION: NOVEL Nucleic Acids and
FILE REFERENCE: 21272-018 (785 contig)
CURRENT APPLICATION NUMBER: US/10/276,781
CURRENT FILING DATE: 2002-11-18
                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 09/491,404
PRIOR FILING DATE: 2000-01-25
NUMBER OF SEQ ID NOS: 2018
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                                                                                                                                                                                                                                                                                                             SOFTWARE:
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GlnargValLeuPheLeuLeuAspGlyTyrAsnGluPheLysProGlnAsnCysProGlu
                         PhePheLeuArgLeuSerArgAlaGlnGlyGlyLeuPheGluThrLeuCysAspGlnLeu
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GENERAL INFORMATION:
APPLICANT: IKEDA, Johe
APPLICANT: SAKAI, Harumi
TITLE OF INVENTION: Monoclonal Antibodies Against Human Apoptosis Inhibitory Protein
TITLE OF INVENTION: and Method For Assaying the NAIP
FILE REFERENCE: 2002-1440/MMC/00653
CURRENT APPLICATION NUMBER: US/10/285,408
CURRENT FILING DATE: 2002-11-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 2
LENGTH: 5984
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PRIOR APPLICATION NUMBER: PCT/JP99/05841
PRIOR FILING DATE: 1999-10-22
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LOCATION: (29
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TTAAAGAATCAGGTCTTATTCCTTTTAGATGACTACAAAGAAATATGTTCAATCCCTCAA
                                                                                                      TTCTACCTCTCCCTTAGTTCCACCAGACCAGACGAGGGGCTGGCCAGTATCATCTGTGAC
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Matches:
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; SEQ ID NO 84
FONCTH: 6133
Sequence 125, Application US/09949002
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 84, Application US/09949002
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
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PRIOR FILING DATE: 2000-01-28
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 10823
SOFTWARE: Factor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/949,002 CURRENT FILING DATE: 2000-01-28
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TYPE: DNA
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                                                                                                                         ATTGCTGTCCGTACAAACAGGGCCAGGGACATCCGCCGATAC
                                                                                                                                                          ValThrThrThrGluCysLeuArgHisIleArgGlnPhe 130
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; LENGTH: 6133
; TYPE: DNA
; ORGANISM: Human
US-09-949-002-125
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; ORGANISM: Human US-09-949-002-656
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GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: AND INFLAMMATORY AUTOIMMUNE DISEASE, A
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL000790
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TENGTH: 6133
                                                                        SEQ ID NO 656
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CURRENT APPLICATION NUMBER: US/09/949,002

CURRENT FILING DATE: 2000-01-28
                                                                                                                          CURRENT APPLICATION NUMBER: US/09/949,002
CURRENT FILLING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: 60/231,401
PRIOR FILING DATE: 2000-09-08
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PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 10823
                                                                                        SOFTWARE: FastSEQ for Windows Version
                                                                                                             NUMBER OF SEQ ID NOS: 10823
                                    TYPE: DNA
                                                   ENGTH: 60194
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; LENGTH: 60195
; TYPE: DNA
; ORGANISM: Human
US-09-949-002-697
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                                 US-09-697-089-2_COPY_161_323 (1-163)
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Query Match:
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GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
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                                                                                                                                                                                                                                                                                                                                                     CURRENT FILING DATE: 2000-01-28
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Conservative:
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US-09-724-676-6819, Application US/09724676

Sequence 6819, Application US/09724676

GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676

CURRENT FILING DATE: 2000-11-28
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SOFTWARE: PatentIn version 3.2
SEQ ID NO 6819
LENGTH: 3210
Type: No.
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AsnCysProGluIleGluAlaLeuIleLysGluAsnHisArgPheLysAsnMetVallle 116
                                                 PhePheLeuArgLeuSer-----ArgAlaGlnGlyGlyLeuPheGluThrLeuCysAsp
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                                                                                                   CAGCTCCTAGAGAAAGAAGGATCTGTTACTGAAATGTGCRTGAGGAACATTATCCAGCAG
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GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
                                                                                                                 Sequence 6801, Application US/09724676 GENERAL INFORMATION:
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LENGTH: 3210
       APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn
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RESULT 12
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US-09-724-676A-6801
Sequence 6801, Application US/09724676A
GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative spl
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 9722
SOFTWARE: PatentIn version 3.2
SOFTWARE: DNA
TYPE: DNA
ORGANISM: Homo sapiens
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US-09-724-676-6801
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LENGTH: 4143
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TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEC ID NOS: 97222
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                                                                      CAGCTCCTAGAGAAAGAAGGATCTGTTACTGAAATGTGCRTGAGGAACATTATCCAGCAG
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     Sequence 6816, Application US/09724676
GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
CURRENT EPILING DATE: 2000-11-28
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TITLE OF INVENTION: Variants of alternative
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILLING DATE: 2000-11-28
NUMBER OF SEO ID NOS: 97222
SOFTWARE: PatentIn version 3.2
NUMBER OF SEQ ID
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ORGANISM: Homo sapiens
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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38: em_sy:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Patent: WO 0190156-A 181 29-NOV-2001;
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/db_xref="GI:17900868"
/db_xref="GI:17900868"
/translation="GRIKHALTKKINDNIKMNEEDAIKLAEGLKNIKKMCLEHLTHLSD
IGEGMDYIVKSLSSEPCDLEEIQLVSCCLSANAVKILAQNLHNLVKLSILDLSENYLE
KDGNEALHELIDRMNVLEQLTALMLPWGCDVQGSLSSLLKHLEEVPQLVKLGIKNWRL
TDTEIRILGAFFGKNPIKMFQQLHLAGNRVSSDGWLAFMGVFENLK"

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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CNRS UPR 420 - Genetique Moleculaire et Biologie du Developeme IFR 1221 - Rue Guy Moquet 19, Batiment G - BP 8 94801 Villejuif Cedex, FRANCE Tel: ++33-1-49 58 34 98 Fax: ++33-1-49 58 35 09 e-mail: auffray@infobiogen.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens mRNA full length AL389934 AL389934.1 GI:9367839
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                                                                                                                                                                                                                                                                                                                                                                                                                      IMPORTANT: This sequence represents the full insert of this IMAGE cDNA clone. No attempt has been made to verify whether this corresponds to the full-length of the original mRNA from which it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Distributors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://www.iro.es e-mail enquiries: lsumoy@iro.es
EURO-IMAGE Consortium Contact: Auffray C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission Submitted (15-JUL-2000) Dept. Genetica Molecular,
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TSLRLQIKRCAGVAGSISLVLSTCKNIYSLAWFASPLTIEDERHITSVTNLKTLSIHD
LQNQRLPGGLTDSLGNLKNLTKLINDIKMNEEDAIKLAEGLKNLKKKCLFHLTHLSD
IGEGMDYIVKSLSSEPCDLEEIQLVSCCLSANAVKILAQNLHNLVKLSILDLSENYLE
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/db_xref="GI:9367840"
/translation="INSGNIPDYLFDFFEHLPNCASALDFIKLDFYGGAMASWEKAAE
                                                                                                                                        musculus
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Damiano, J.S., Stahlik, C., Pio, F., Gc Clan, a novel human ced-4-like gene Genomics 75 (1-3), 77-83 (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
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/note="LRR;
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Poyet, J.L., Srinivasula, S.M., Tnani, M., Razmara, M., Fernandes-Alnemri, T. and Alnemri, E.S.
Identification of Ipaf, a human caspase-1-activating related to Apaf-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (16-MAY-2001) Microbiology and Immunology, The Jefferson University, 233 S. 10th Street, Philadelphia,
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MKTPLEVVITCAIGMGESEEHSHTGTTLFHTFYDLLICKKKKKIKIKGVAASDFIRSLDH
GGDLALEGVFSHKFDFELGDVSSVNEDPLLTTGLLGICKYTAORFKRYKFFHKSTGESLDH
GGDLALEGVFSHKFDFELGDVSSVNEDPLLTTGLLGICKYTAORFKRYKFFHKSTGESLDH
AGRRLSSLLTSHEPEENTKGNGYLQKMYSISDITSTYSSLLRYTGGSSVEATRAVMKH
LAAVVOHGCLLGLSLAKRPLWRGESLGSVKNTTEDEILKAININSFVEGCIHLYODST
SKSALSQEFEAFFGGKSLYINGGNIPDYLFDFFFHLPNCASALDFIKLDFYGGAMASW
EKAAEDTGGIHHEEAPETYIPSTAVSLFFNWKOEFRTLEVTLRDFSKLNKODIRYLGK
IFSSATSLRIGIKRCAGVAGSLSLVLSTCKNIYSLMVEASPLTIEDERHITSVTMLKT
LSIHDLQNQRLPGGLTDSLGNLKNLTKLIMDNIKMNEEDAIKAAEGLKNLKKMCLFHL
THLSDIGEGMDYIVKSLSSEPCDLEEIGLVSCCLSANAVKILAQMIRNLVKLSLIDLS
ENYLEKDGNEALHELLDRMNVLEQLTALMLPWGCDVGGSSLSLLKHLEEVPQLVKLGL
KNWRLTDTEIRILGAFFGKNPLKNFQQLNLAGNRVSSDGWLAFMGVFENLKQLVFFDF
STKEFLEDDALVKKLSQVLSKLTFLQERRLVGMQFDDDDLSVITGAFKLVTA"

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LQSPCIIEGESGKGKSTLLQRIAMLWGSGKCKALTKFKFVFFLRLSRAQGGLFETLCD
QLLDIPGTIRKQTFMAMLLKLRQRVLFLLDGYNEFKPQNCPEIEALIKENHRFKNMVI
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KVEQDAARGIIHMILKKGSESCNLFLKSLKEWNYPLFQDLNGQSLFHQTSEGDLDDLA
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/protein_id="AAK59843.1"
/db_xref="GI:14334215"
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                                                                                                                                                                                                                                   Homo sapiens, caspase recruitment domain MGC:35330 IMAGE:5179909, mRNA, complete c BC031555 BC031555.1 GI:21594975 MGC.
CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Baylor College of Medicine Human Genom Sequencing Center
                                               Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies,
                                                                       NIH-MGC Project URL: http://mgc.nci.nih.Contact: MGC help desk
                                                                                                   USA
                                                                                                                                                 Direct Submission
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This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
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Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Huly
Yoon, Y.S., Kowis, C.R., Lawrence, S., Mart
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LQSPCITEGESGKGKSTLLQRIAMLWGSGKCKALTKEKFFFERLSRAQGGLFETLCD
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KNWRLTDTEIRILGAFFGKNPLKNEGOLNLAGGNRVSDGWLAFMGVFENLKÖLVFEDF
KANRLTDTEIRILGAFFGKNPLKNEGOLNLAGGNRVSSDGWLAFMGVFENLKÖLVFEDF
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/protein_id="AAH31555.1"
/protein_id="AAH31555.1"
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1 718 c 768 g 863 t
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/tissue_type="Brain, Lung, Testis,
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/db_xref="taxon:9606"
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Patent: WO 0190156-A 96 29-NOV-2001;
The Burnham Institute (US)
Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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/db_xref="taxon:9606"
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Homo sapiens CLANA (CLAN1) mRNA,
AY027787
AY027787.1 GI:14324112
Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 3396)
Damiano, J.S., Stehlik, C., Pio, F., Godzik, A. and Reec Clan, a novel human ced-4-like gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Stehlik, C., Damiano, J.S., Pio, F., Godzik, A. and Reed, J.C
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KNWRLTDTEIRILGAFFGKNPLKNFQQLNLAGNRVSSDGWLAFWGVFENLKQLVFFDF
STKEFLPDPALVRKLSQVLSKLTFLQEARLVGWQFDDDDLSVITGAFKLVTA"
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VTTTECLRHIROFGALTAEVGDMTEDSAQALIREVLIKELAEGLILJOJOKSRCLRNL
MKTPLFVVITCA IQMGESEFHSHTQTTLFHTEYDLLICKKHKHKKGVAASDEIRSLDH
RGDLALEGVFSHKFDELQDVSSVNEDVLLTTGLLCKKTAQREKFKKKFHKSSFQEYET
RGRRLSSLLTSHEPEBVTKGNGYLQKMVSISDITSTYSSLLRYTCGSSVEATRAVMKH
LAAVKYHGCLLGLSIAKRPLMRQESLOSVKNTTEGEILKAININSFVECGIHLYQEST
SKSALSQEFEAFFGKKSLYINSGNIDDYLFDFEHLFURSALDFIKLDFYGGAMASH
EKAAEDTGGIHMEEAFETYIPSRAVSLFFNWKGEFRTLEVTLKDFSKLNKQDIRYLGK
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QDLKDLYHTPSFLNFYPLGEDIDIIFNLKSTFTEPILWRKDQHHHRVEQLTLNGLLQA
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/db_xref="GI:14324113"
/translation="MNFIKDNSRALIQRMGMTVIKQITDDLFVWNVLNREEVNIICCE
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/note="alternatively spliced;
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1 (bases 1 to 3581)
Gingras, M.-C., Qiu, J. and Margolin, J.F.
Gingras, M.-C., Qiu, J. and Margolin, J.F.
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Gingras, M.-C., Qiu, J. and Margolin, J.F.
Direct Submission
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                                                                                                                        /product="caspase recruitment domain protein 12"
/protein_id="AAK33443.1"
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ODLKDLYHTESFLNYYLGEDDLDIINMLKSTFTEFVLWRKDOHHRVEDUTLNGLLQA
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ODLKDLYHTESFLNYYLGEDDLDIINMLKSTFTLEVLWRKSTFYFFLRLSRAQGGLFETLCD
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                                               VTTTTECLRHIRQFGALTAEVGDMTEDSAQALIREVLIKELAEGLLLQIQKSRCLRNL
MKTPLFVVITCAIQMGESEFHSHTQTTLFHTFYDLLIQKNKHKHKGVAASDFIRSLDH
AGRRLSSLLTSHEPEEVTKGNGYLQKMVSISDITSTYSSLLRYTCGSSVEATRAVMKH
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                                                                                                                                                                                                                                                                                                                                                                                                                                   /map="2p21-22"
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RESULT 11
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                                                                                                                                                         GluAsnLeuLys
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                                                                                                                                                                                             TTGAATTTGGCGGGAAATCGTGTGAGCAGTGATGGATGGCTTGCCTTCATGGGTGTATTT
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AK095467 3355 bp mRNA linear Homo sapiens cDNA FLJ38148 fis, clone D9OST2003791, to Homo sapiens ICE-protease activating factor mRNA
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SKSALSQEFEAFFQGKSLYINSGNIPVYLFDFFEHLPNGASLDFIKLDFYGGAMASW
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KNWRLTDTEIRILGAFFGKNPLKNFQQLNLAANRVSSDGWLREMGVFENIKQVFFDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Region: caspase recruitment domain"
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GlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeuGlu 100
                                                                   LeuGluGluIleGlnLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeuAla 80
                                                                                                                                                                                                                                              LysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHisLeu
                                                                                                                                   TCTGACATTGGAGAGGGAATGGATTACATAGTCAAGTCTCTGTCAAGTGAACCCTGTGAC
                                                                                                                                                          SerAspIleGlyGluGlyMetAspTyrIleValLysSerLeuSerSerGluProCysAsp|
                                                                                                                                                                                                                         AAACTAGCTGAAGGCCTGAAAAACCTGGAGAAGATGTTTATTTCATTTGACCCACTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (04 JUL-2002) Takao Isogai, FLJ Project(HRI Team); 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan RAY Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.
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Isogai,T. and Yamamoto,J.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ninomiya,K., Wagatsuma,M., Kanda,K., Kondo,H., Yokoi,T., Kodaira,H., Furuya,T., Takahashi,M., Kikkawa,E., Omura,Y., Abe,K. Kamihara,K., Katsuta,N., Sato,K., Tanikawa,B., Yamazaki,M., Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Wakamatsu,A., Ishii,S., Yamamoto,J., Isono,Y., Kawai-Hio,Y., Saito,K., Nishikawa,T., Yamashita,H., Matsuo,K., Nakamura,Y., Sekine,M., Kimura,K., Yamashita,H., Matsuo,K., Nakamura,Y., Sekine,M., Kikuchi,H., Murakawa,K., Kanehori,K., Nakamura,Y., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S., Nagahari,K., Masuho,Y., Nagai,K. and Isogai,T. Nagahari,K., Masuho,Y., Nagai,K. and Isogai,T.
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Homo sapiens CD34+ Cells cDNA to mRNA, clone_lib:D9OST2 clone:D9OST2003791.
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1 726 c
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after 9-days ODF induction.-primary culture, CD34+ Cells"
726 c 774 g 869 t
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/db_xref="taxon:9606"
/clone="D9OST2003791"
/cell_type="CD34+ Cells"
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Submitted (18-APR-2002) Genoscope - Centre National de Se
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genosco
- Web : www.genoscope.cns.fr)
On Mar 6, 2000 this sequence version replaced gi:6002386.
Location/Qualifiers
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Spastin, a novel AAA protein, of autosomal dominant spastic
Nat. Genet. (1999) In press
2 (bases 1 to 138909)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequencing vector: M13; 57% Sequencing vector: plasmid; 40% Chemistry: Dye-primer ET; 48% of reads Chemistry: Dye-terminator Big Dye; 50% of reads Assembly program: Phrap; version 0.990319
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Waterston, R.H.
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                 1. .185281
2086. .8183
/note="assembly_name:Contig12"
8284. .22741
                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                    Location/Qualifiers
                                                                /note="assembly_name:Contig11"
                                                                                                            /clone="RP11-78E13"
                                                                                                                                   chromosome="2"
                                                                                                                                                                                                                                      1985: contig of 1985 bp in length
2085: gap of unknown length
8183: contig of 6098 bp in length
8283: gap of unknown length
22741: contig of 14458 bp in length
22841: gap of unknown length
41446: contig of 18605 bp in length
41546: gap of unknown length
69182: contig of 27636 bp in length
69282: gap of unknown length
112131: contig of 42849 bp in length
11231: gap of unknown length
11658: contig of 73050 bp in length.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Db 171729 GCTCAGAATCTTCACAATTTGGTCAAACTGAGCATTCTTGATTTATCAGAAAATTACCTG
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       171549 ATACCCATGTGTGCCTTACTAGATGCACCCTCCTTAGGAAAATCATTTAGGCCCTTTCTTA 171490
171009 TTCCTCAGTTTTGAGACCATCCAGTCCCTGAACTGCTCTTTGTTTCTTCCAGTCGACAGG 170950
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                                                                                       TGAGTAGGCTGCAGAGCCACCAAACATAAAGATCATTCCTCCCCTAACACCCCTTTGTTC 171010
                                                                                                                                                                             GTATATGCTTGAATACTTTCCAAAAAAAAAACCAAAAATTAAGTAGATTCTCATTACAGAT 171070
                                                                                                                                                                                                                                                                                                                                                       TGCTTTAGAATAATACAGGAGGAATTAGGTCAGGATTAAGCAACATTGCCCCATGATTTAA 171190
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                                                                                                                                                                                                                                                                    TGTTTTTGAAGGTGTCTTATTAGTATATATAGTTTCATTATATTCTTCTGCATAATGTTT
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22842. .41446
/note="assembly_name:Contig14"
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112232, .185281
/note-"assembly_name:Contig17"
/36957 c 37187 g 57816 t
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AC010968
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                                                                                                                                                                                                                                             Sequencing vector: M13; 598
Sequencing vector: M13; 598
Sequencing vector: Plasmid; 418
Chemistry: Dye-primer ET; 478 of reads
Chemistry: Dye-terminator Big Dye; 538 of reads
Assembly program: Phrap; version 0.99319
Consensus quality: bases at least Q30
Consensus quality: bases at least Q30
Consensus quality: bases at least Q20
Insert size: 147000; agarose-fp
Ouality coverage: 6.64 in Q20 bases; sum-of-contigs
Quality coverage: 6.38 in Q20 bases; sum-of-contigs
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Homo sapiens chromosome 2 clone
11 unordered pieces.
AC010968
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Submitted (28-SEP-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
MO 63108, USA
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Waterston, R.H.
The sequence of Homo sapiens clone
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Mammalia; Eutheria;
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HTG; HTGS_PHASE1; HTGS_DRAFT
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                                                                       arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                   NOTE: This is a 'working draft' sequence. It currently consists of 11 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Aug 18,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (bases 1 to 160583)
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 1080: contig of 1080 bp in length
1180: gap of unknown length
2476: contig of 1296 bp in length
2576: gap of unknown length
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Primates;
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RP11-9302,
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US-09-697-089-2_COPY_762_965 (1-204) x AC010968 (1-160583)
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                                                  GAAAAAGATGGAAATGAAGCTCTTCATGAACTGAGTAAGAATGACAATTCAGCCAAAATT 64567
AGATACTTGAATATGTATACTGGGTAGTCGAAATACATAGCCTGGGGTCCTGAGGTCTTTT 64627
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/note="assembly_name:Contig21"
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65623. .91498
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91599. .116835
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/db_xref="taxon:9606"
/chromosome="2"
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9707. .17078
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        Eukaryota; Metazoa; Chordat
Mammalla; Eutheria; Primate
1 (bases 1 to 553)
Olivier, M. and Cox, D.R.
Unpublished, Olivier, M., C
Unpublished (2000)
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Best Local Similarity:
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79
                                           Contact: Michael Olivier, David R. Cox Stanford Human Genome Center Stanford University School of Medicine 4005 Miranda Ave. 2nd Fl., Palo Alto, CA Tel: (650) 320-5800 Fax: (650) 320-5801 Email: Olivier@shgc.stanford.edu primer A: AATAAGGGGGCAAAATAACCAAA primer B: TAACACCCCTTTGTTCTTCCTCA STS size: 322 PCR Profile:
                                                                                                  ValGlnGlySerLeuSerSerLeuLeuLysHisLeuGluGluValProGlnLeuValLys 150
CATACAGAGCCAAGATAACTGGATTTGGCCCCTTAAAAAATTC
                      GlyLysAsnPro----
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-DB-W_Geneseq_101002 -QFWMT-fastap -SUFFIX-ep2n.rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS-bits -START=1 -END=-1 -MATRIX-blosum62 -TRANS-human40.cdi
-LIST=45 -DCCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-LOCAL-CCAL-OUTFMT-pto -NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER-US09697089_@CGN_11_1276_@runat_29012003_092753_19709 -NCPU-6 -ICPU-3
-NO.XIPXY -NO.MMAP -LARGEQUERY -NEG_SCORES-0 -WAIT -LONGLOG -DEV_TIMEDUT=120
-WARN_TIMEDUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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Fgapop 6.0 , Fgapext
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Caspase recruitment domain; CARD; ss; NB-ARC; ANGIO-R; LRR; SAM; abnormal cell proliferation; cancer; abnormal cell death; apoptosis; autoimmune disease; inflammation; keratinocyte hyperplasia; inflammatory hyperplasia; fibrosis; smooth muscle cell proliferation; balloon angioplasty; restenosis; glioma; carcinoma; sarcoma; melanoma; leukaemia; altergy; arthritis; lupus; Schrogen's syndrome; Crohn's disease; graft-versus-host disease; stroke; myocardial infarction; heart failure; neurodegenerative disease;
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10-OCT-2000;
14-MAR-2001;
23-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                              pathology characterised by abnormal cell proliferation (e.g. cancer), abnormal cell death (apoptosis), autoimmune diseases or inflammation. In particular, the polypeptide and nucleic acid are useful for treating keratinocyte hyperplasia, inflammatory hyperplasia, fibrosis, smooth muscle cell proliferation in arteries following balloon angioplasty (restenosis), gliomas, carcinomas, sarcomas, melanomas, leukaemias, allergies, arthritis, lupus, Schrogen's syndrome, Crohn's disease, graft-versus-host disease, stroke, myocardial infarction, heart failure, neurodegenerative diseases (e.g. Parkinson's disease or Alzheimer's disease) or immunodeficiency virus (HIV) infection). The nucleic acids are useful in a variety of diagnostic applications. The present sequence is a contact.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  encoding nucleic actus, cornell death, autoimmune diseases arthritis or stroke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an isolated caspase recruitment domain (CAR containing polypeptide, or a CARD, NB-ARC, ANGIO-R, LRR or SAM dome from it, and the polynucleotides encoding them. Also included are a recombinant vector comprising the polynucleotide, recombinant cells
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             containing the vector (e.g. bacteria, yeast, plant, animal, mammali and insect cells) and an anti-CARD antibody. The CARD-containing polypeptide and CARD-encoding nucleic acid are useful for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New caspase recruitment domain (CARD)-containing polypeptides and encoding nucleic acids, useful for treating abnormal cell prolife or cell death, autoimmune diseases or inflammation, e.g. carcinometers.
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24-MAY-2000;
10-OCT-2000;
14-MAR-2001;
23-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                 Caspase recruitment domain; CARD; ss; NB-ARC; ANGIO-R; LRR; SAM; abnormal cell proliferation; cancer; abnormal cell death; apoptosis; autoimmune disease; inflammation; keratinocyte hyperplasia; inflammatory hyperplasia; fibrosis; smooth muscle cell proliferation; balloon angioplasiy; restenosis; glioma; carcinoma; sarcoma; melanoma; leukaemia; allergy; arthritis; lupus; Schrogen's syndrome; Crohn's disease; graft-versus-host disease; stroke; myocardial infarction; heart failure; neurodegenerative disease; myocardial infarction; heart failure; neurodegenerative disease;
                                                                                                                                                                                                                                                                                                                                   Parkinson's disease; Alzheimer's disease; human immunodeficiency virus infection.
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2000US-0686347.
2001US-275980P.
2001US-0864921.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polypeptide and CARD-encoding nucleic acid are useful for treating a capacitology characterised by abnormal cell proliferation (e.g. cancer), and abnormal cell death (apoptosis), autoimmune diseases or inflammation. In particular, the polypeptide and nucleic acid are useful for treating CC keratinocyte hyperplasia, inflammatory hyperplasia, fibrosis, smooth cmuscle cell proliferation in arteries following balloon angioplasty CC (restenosis), gliomas, carcinomas, sarcomas, melanomas, leukaemias, ca llargies, arthritis, lupus, Schrogen's syndrome, Crohn's disease, CC allergies, arthritis, lupus, Schrogen's syndrome, Crohn's disease, CC (araft-versus-host disease, stroke, moyocardial infarction, heart failure, CC (amunodeficiency attroke, moyocardial infarction, heart failure, CC (alsease) or immunodeficiency associated disease (e.g. human CC (alsease) or immunodeficiency associated disease (e.g. human CC (alsease) or immunodeficiency associated disease (e.g. human CC (cc) availety of diagnostic applications. The present sequence is a CC (cDNA encoding a CARD domain containing protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     recombinant vector comprising the polynucleotide, recombinant cells
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                                                 ThralaLeuMetLeuProTrpGlyCysAspValGlnGlySerLeuSerSerLeuLeuLys 140
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Conservative:
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         AAH99166 to AAH99904 encode the human proteins given in AAM25225 to AAM25963. The proteins can have activities based on the tissues and cells they are expressed in, such as: antiinflammatory; antirheumatic; antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant; central nervous system; virucide; anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; antiaggregant; haemostatic; vulnerary; antiplicer; osteopathic; dermatological; antiallergic; antiasthmatic;
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21-JAN-2000;
25-APR-2000;
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antidiabetic; cytostatic; neuroprotective;
                                                                                                                                        Claim
                                                                                                                                                                  Isolated human polynucleotides encoding treatment and diagnosis of e.g. cancer,
                                                                                                                                                                                                                   P-PSDB;
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Matches:
Conservative:
Mismatches:

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Alignment

Scores

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The sequence represents a cDNA which encodes the human caspase or recruitment domain 12 (CARD-12) polypeptide. CARD domains are found in a CC number of proteins that transmit signals that activate apoptosis and CC inflammatory pathways in response to stress and other stimuli. Therefore, CC CARD-12 and its corresponding nucleic acid may be used in treatment and CC diagnosis of patients suffering from disorders associated with an CC abnormal level (an increase or a decrease) of apoptotic cell death or abnormal activity of stress-related pathways. The disorders include CC cancer, viral infections (e.g. caused by poxviruses, adenoviruses), cutoimmune disorders (e.g. systemic lupus crythematosis, arthritis), cc neurological disorders (e.g. Alzheimer's disease, amyotrophic lateral CC sclerosis), haematologic diseases (e.g. aplastic anaemia, myocardial cinfarction, stroke), inflammatory and immune system disorders (e.g. Sclerosis), stroke), inflammatory and immune system disorders (e.g. sclerosis), inflammatory and immune system disorders (e.g. coused by contact dermatitis, cc contact leprosy), ischaemic and hypoxic brain injury, kidney contact screenia/reperfusion injury, excitotoxic brain damage, acute bacterial cc meningitis and liver disease.
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                                                                              Human; secreted polypeptide; nervous disease; muscular disease; tumour; gastrointestinal ulceration; spinal cord disease; trachea disease; thyroid gland disease; ovary disease; prostate disease; heart disease; renal gland disease; small intestine disease; thymus disease; muscular system disease; colon disease; lymph node disease; muscular system disease; colon disease; lipase deficiency; cystic fibrosis; pancreatitis; clot formation; myocardial infarction; angioplasty; liver disease; coagulation disorder; microbial disease; immune disorder; inflammation; transplant rejection; bone thickness; bone density; ferroxidase loss; apoptosis; vascular smooth cell proliferation; vaccine; ss.
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Alignment
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Best Local Similari
                                                                                                                                                                                                                                                                                                                                                                The present sequence encodes a human secreted polypeptide. The CC secreted polypeptides and polynucleotides are useful for treating CC nervous and muscular diseases, for inhibiting tumour formation and CC metastasis, for treating gastrointestinal ulceration, for preventing CC and treating diseases in spinal cord, thyroid gland, ovary, prostate, CC renal gland, small intestine, heart, trachea, thymus, lymph node, CC muscular system and colon, for treating lipase deficiency in cystic CC fibrosis and pancreatitis, for treating undesirable clot formation CC such as myocardial infarction, during angioplasty and all surgical CC procedures that require decreased blood clot formation, for treating CC iver diseases, coagulation disorders and microbial diseases, for CC treating immune disorders, for treating inflammation and transplant CC rejection, for enhancing bone thickness and increasing bone density, CC apoptosis, and for regulating vascular smooth cell proliferation. They CC may also be used as vaccines.
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03-OCT-2000;
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                                                    SerAspIleGlyGluGlyMetAspTyrIleValLysSerLeuSerSerGluProCysAsp
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 New caspase recruitment encoding nucleic acids,
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cc recombinant vector comprising the polynucleotide, recombinant cells containing the vector (e.g. bacteria, yeast, plant, animal, mammalian cand insect cells) and an anti-CARD antibody. The CARD-containing cand insect cells) and an anti-CARD antibody. The CARD-containing cc polypeptide and CARD-encoding nucleic acid are useful for treating a pathology characterised by abnormal cell proliferation (e.g. cancer), cc abnormal cell death (apoptosis), autoimmune diseases or inflammation. In cc particular, the polypeptide and nucleic acid are useful for treating cc keratinocyte hyperplasia, inflammatory hyperplasia, fibrosis, smooth cc muscle cell proliferation in arteries following balloon angioplasty cc (restenosis), gliomas, carcinomas, sarcomas, melanomas, leukaemias, cc allergies, arthritis, lupus, Schrogen's syndrome, Crohn's disease, cc graft-versus-host disease, stroke, myocardial infarction, heart failure, cc allergies, arthritis disease, stroke, myocardial infarction, heart failure, cc meurodegenerative diseases (e.g. Parkinson's disease or Alzheimer's cc alsease) or immunodeficiency virus (HIV) infection). The nucleic acids are useful con a variety of diagnostic applications. The present sequence is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to an isolated caspase recruitment domain (CARD) containing polypeptide, or a CARD, NB-ARC, ANGIO-R, LRR or SAM domain from it, and the polynuclectides encoding them. Also included are a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          arthritis or stroke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cell death, autoimmune diseases or inflammation,
                                               encoding a CARD
                                                     domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              216pp;
                                                  containing protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    English.
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Percent Similarity: Best Local Similarity: US-09-697-089-2_COPY_762_965 (1-204) Query Match: Alignment No. Scores: 1.09e-105 1046.00 100.008 100.008 100.008 100.008 x ABK22731 (1-3396) Conservative: Mismatches: Indels: Gaps: Length: Matches: 3396 204 0 0 0

Sequence 3396 BP;

992 A; 737 C;

793 G; 874 T; 0 other;

밁 QΥ 밁 δÃ 2560 21 LeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluGluAspAlaIle LysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHisLeu 2679 40 2619 20

2620 AAACTAGCTGAAGGCCTGAAAAACCTGAAGAAGATGTGTTTATTTCATTTGACCCACTTG

101 120

Qy В Ωy 밁 Ş 밁 δÃ

Qy В 2860 121 2919

밁 ThrAlaLeuMetLeuProTrpGlyCysAspValGlnGlySerLeuSerSerLeuLeuLys ACCGCACTGATGCTGCCCTGGGGCTGTGACGTGCAAGGCAGCCTGAGCAGCCTGTTGAAA 140 2979

밁 Ωy 2980 141 HisLeuGluGluValProGlnLeuValLysLeuGlyLeuLysAsnTrpArgLeuThrAsp CATTTGGAGGAGGTCCCACAACTCGTCAAGCTTGGGTTGAAAAAACTGGAGACTCACAGAT 3039 160

밁 Qy 3040 161 ThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPheGlnGln ACAGAGATTAGAATTTTAGGTGCATTTTTTGGAAAGAACCCTCTGAAAAACTTCCAGCAG 3099 180

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RESULT 7
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                                                                                       US-09-697-089-2_COPY_762_965 (1-204) x AAH98254
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                                                                                                                                                                                                                                                     Percent Similarity:
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17-JUL-2000;
03-AUG-2000;
15-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention provides the protein and coding sequences of novel proteins from a variety of organisms, including human, dog, cat, horse, cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea urchin and tomato. These were derived from expressed sequence tags (ESTs) from the organism of interest. They can be used in diagnostics, forensics, gene mapping, identification of mutations, to assess biodiversity and for nutritional purposes. The present sequence is a cDNA for the present sequence of the present sequence is a cDNA for the present sequence of the present sequence of the present sequence is a cDNA for the present sequence of the present sequence of the present sequence is a cDNA for the present sequence of the present sequence of the present sequence of the present sequence of the present sequence of the present sequence of the present sequence of the present sequence of the present sequence of the present sequence of the present sequence of the present sequence of the present sequence of the present sequence of the present sequence of the present sequence of the present sequence of the present sequence of the present sequence of the present sequence of the present sequence of the present sequence of the present sequence of the present sequence of the present sequence of the present sequence of the present sequence of the present sequence of the present sequence of the present sequence of the present sequence of the present sequence of the present sequence of the present sequence of the present sequence of the present sequence of the present sequence of the present sequence of the present sequence of the present sequence of the present sequence of the present sequence of the present sequence of the present sequence of the present sequence of the present sequence of the present sequence of the present sequence of the present sequence of the present sequence of the present sequence of the present sequence of the present sequence of the present sequence of the present sequence of the pres
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tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
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                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3545
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gene mapping; genetic disorder;
nutrition; ss.
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                                                                                                                                                           cancer; viral infection; poxvirus; adenovirus; autoimmune disorder; systemic lupus erythematosis; arthritis; neurological disorder; stroke; Alzheimer's disease; amyotrophic lateral sclerosis; haematologic disease; aplastic anaemia; myocardial infarction; inflammatory disorder; crohn's disease; insulin-dependent diabetes; contact dermatitis; psorlasis; graft rejection; bacterial infection; lepromatous leprosy;
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                                                                                                                                                                                                                                 Caspase recruitment domain; CARD-12; apoptosis; stress-related pathway;
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                                            "Human CARD-12"
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Best Local Similarity:
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      CC cancer associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, CC diagnosis and treatment of diseases associated with inappropriate P CC expression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions CC in a patient's genome that affect the activity of P by expressing CC inactive proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer-associated Ps, by inserting the nucleic acids into a host cell and culturing the cell course of the proteins. N and P can be used in the prevention, diagnosis and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204 and AAB7789 represent sequences used in the exemplification of the
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and/or treating colorectal cancers -
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26-MAY-2000;
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                                                                                                                                                                                                                                                                                                                         Human breast cell single exon nucleic acid probe #4307
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                                                                                                                                                                                                                                                                             disease;
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                                                                                                                                               30-JAN-2001; 2001WO-US00662
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                                                                                                                                                                                                                                                                                          microarray;
                                                                                                                                                                                                                                                                             cancer;
                            2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
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                                                                                                                                                                                                                                                                                          single exon probe;
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RESULT 11
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26-MAY-2000;
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                                                                                                               WO200157277-A2
                                                                                                                                                                            Human;
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Alignment Scores:
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                                                                                                                                                                rapid production of functional information from genomic sequence. The present sequence is a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     from human breast and BT 474 cells. The method involves contacting the probes with a collection of detectably labelled nucleic acids
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                                                                Sequence 421
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                                                                   BP; 126 A;
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US-09-697-089-2_COPY_762_965 (1-204) x ABA45612 (1-421)
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Best Local Similarity:
                                                                                                                  Query Match:
ABA56119 standard;
                             2.49e-13
202.00
100.00%
100.00%
19.31%
22
DNA; 421
ВP
                                                                                                                 Conservative: Mismatches: Indels:
                                                                                                                                       Length:
Matches:
                                                                                                         00008
                              294
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foetal liver single exon nucleic acid probe #4424

(first entry)

foetal

liver;

gene expression; single

exon

nucleic

acid probe;

SS

2000US-0180312 2000US-0207456 2001WO-US00669

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Best Local Si
Query Match:
DB:
 RESULT 12
ABA2570
ABA2570
ABA2570
AC ABA2
XX ABA2
XX Prob
XX Huma
XX Card
CT Card
CX Card
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03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
 04 - FEB - 2000;
26 - MAY - 2000;
30 - JUN - 2000;
03 - AUG - 2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention.
                                                                                      30-JAN-2001; 2001WO-US00666
                                                                                                                           09-AUG-2001
                                                                                                                                                             WO200157274-A2
                                                                                                                                                                                               Homo
                                                                                                                                                                                                                                congenital heart disease;
                                                                                                                                                                                                                                                human; gene expression;
cardiovascular disease;
                                                                                                                                                                                                                                                                                                                                                                          ABA25770;
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; 2000US-0632366.
; 2000US-0234687.
; 2000US-0236359.
; 2000US-0024263.
 2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
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Matches:
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cardiac arrhy
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DB:
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04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
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                                                                                                       09-AUG-2001
                                                                                                                                                                                                            epilepsy;
                                                                                                                                                                                                                                                                                 Human
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US-09-697-089-2_COPY_762_965 (1-204) x ABA25770
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27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart. The present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular systems, cardiovascular disease, hypertension, cardiac arrhythmias and e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
                                                                                                                                                                              microarray; Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Note: The sequence data for this patent did not form specification, but was obtained in electronic format at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                            WO200157275-A2
                                                                                                                                                                                            Human; brain expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               congenital heart disease.
                                                      30-JAN-2001;
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                                                                                                                                                                                                                                                                                                         standard;
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2000US-0207456.
2000US-0608408.
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Mismatches:
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Query Match:
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                    04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the
                                                                                                                                                                                              30-JAN-2001;
                                                                                                                                                                                                                                        09-AUG-2001
                                                                                                                                                                                                                                                                              WO200157276-A2
                                                                                                                                                                                                                                                                                                                                                                                     Human; bone
                                                                                                                                                                                                                                                                                                                                                                                                                             Human bone marrow expressed single exon probe SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-NOV-2001
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lymphoma; myeloma;
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                                                                                                     04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                            30-JAN-2001; 2001WO-US00670
                                                                                                                                                                                                                                                           09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                   cervical cancer;
                                                                                                                                                                                                                                                                                                                                                                  Probe; human;
                                                                                                                                                                                                                                                                                                                                                                                             Probe #4322 for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAI14389;
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the probes of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             genome-derived single exon nucleic acid probes useful ting gene expression in human bone marrow -
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                                                                        MOLECULAR DYNAMICS
                                            Hanzel DK,
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                                                                                                     2000US-0180312.
2000US-0207456.
2000US-068408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
2000US-0236359.
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Search completed: January 31, Job time: 245.662 secs
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to human single exon nucleic acid probes (SENP). The present sequence is one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 421 BP; 126 A; 69 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                       25; SEQ ID No 4322; 487pp; English.
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Copyright
GenCore version 5.1.3 (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| | | 0 00 | Result No. |
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| 444443333554322222222222222222222222222 | 9870 | 70 W 4 D V | 1 . |
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ALIGNMENTS

DEFINITION ACCESSION VERSION RESULT 1 AV719179/c LOCUS REFERENCE SOURCE ORGANISM KEYWORDS AUTHORS l (bases 1 to 480)
Olan, B., Wu,T., Huang,Q., Huang,C., Kang,B., Gao,X., Xu,Z., Xiao,H.,
Xu,X., Li,N., Peng,Y., Liu,F., Qu,J., Song,H., Cheng,Z., Zeng,L.,
Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu,G., Yang 480 bp mRNA linear EST 16-OCT-2000 AV719179 GLC Homo sapiens cDNA clone GLCEQA10 5', mRNA sequence. AV719179 AV719179 GI:10816331 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 480) EST Homo sapiens Hominidae; Euteleostomi;
Homo.

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Eukaryota; Metazoa; (
Mammalia; Eutheria; I
1 (bases 1 to 775)
         NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
Unpublished (1999)
Contact: Robert Strausberg, Ph.D
                                                                                                                                                          BI854236
603381263F1 NCI_CGAP_Mam4
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                                                                                                                 EST
                                                                                                                                       mRNA sequence.
BI854236
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This clone is available at CHGC
Location/Qualifiers
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Email: hanzg@chgc.si
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Contact: Zeguang H
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                                                                                                      house mouse
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cgapbs-r@mail.nih.gov
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XhoI"
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/dev_stage="Adult"
/lab_host="SOLR"
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/clone_lib="GLC"
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/db_xref="taxon:9606"
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western clawed frog
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Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                          mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium
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                                                                                            XGC-neurula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="NCI_CGAP_Mam4"
tissue_type="tumor, gross tissue"
/dev_stage="5 months"
/lab_host="DH10B"
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/clone="IMAGE:5389239"
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                                                                                                                                                    CAAGAAGGGAAGGAATCAGTAGAAGAACTGGCTGCCAACTTGACTTATCTTGATGCAATA
                                                                                                                                                                                     LysaspGlyasnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGluGlnLeu
                                                                                                                                                                                                                                                 GlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeuGlu
                                                                                                                                                                                                                                                                                                      CTTAAAGAACTGAAATTAATTGACTGTTGTTTGAGTGTGAAAGCTCTCATGAGTCTTGCA
                                                                                                                                                                                                                                                                                                                            LeuGluGluIleGlnLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeuAla 80
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 ACATTGAGGCGCATTCCTACCTTGTCAGAACTTGCTTTTAAACGATGGAACTTGACCAAT
                                                                                                            ThrAlaLeuMetLeuProTrpGlyCysAspValGlnGlySerLeuSerSerLeuLeuLys
                                                                                                                                                                                                                           TTCCGCTTAAAAATGTTCTCTAGCATTGAAATATTGGATTTGTCTGGAAATTATTTACTA 432
                                                                                                                                                                                                                                                                                                                                                                                 TCCAACATTGGAGATGGCATGGAGAGTATTGCAGAATCAATTTCCTTATGTTGCCATGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sanger Xenopus tropicalis EST project 2001
TROPICALIS_SEQUENCE_ID: TNeu076a12.plcSP6
Sequencing primer: plCSP6
This sequence is from a Xenopus Gene Collection (XGC) library constructed by Aaron M. Zorn.
Location/Qualifiers
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Sanger Centre
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: trop@sanger.ac.uk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="XGC-neurula"
/dev_stage="neurula"
/lab_host="Escherichia coli DH10B"
/lab_host="Escherichia coli DH10B"
/note="Vector: pCS107; Site_1: EcoRI, Site_2: NotI; cDNA
/note="Vector: pCS107; Site_1 = CORI, A from neurula
was oligo dT primed from Sug of poly A RNA from neurula
EcoRI-NotI cut cDNA was then ligated into pCS107 with
EcoRI-at the 5', end and NotI at the 3' end."
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/db_xref="taxon:8364"
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                  LeuGlyLeuLysAsnTrpArgLeuThrAspThrGluIleArgIleLeuGlyAlaPhePhe
                                                                                        ValGlnG1ySerLeuSerSerLeuLeuLysHisLeuGluGluValProGlnLeuValLys
                                                                                                                                             GTCGACAGGATGAACGTGCTAGAACAGCTCACCGCACTGATGCTGCCCCTGGGGGCTGTGAC
                                                                                                                                                              GATGACTTGATGACATTAGCTTCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Shaying Zhao, William Nierman, Mark Adams Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and Venter,J.C. Use of human BAC End Sequences for Sequence-Ready Map Building
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1998)
Other_GSSs: RPCI11-93C9.TJ
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Clones are derived from the human BAC library RPCI-11. For
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 301 838 0200 Fax: 301 838 0208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                               /cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1:
/RPCIll Human Male BAC Library"
a 107 c 114 g 162 t
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/db_xref="GDB:7535384"
/db_xref="taxon:9606"
/clone="RPCI-11-93C9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="RPCI-11"
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BQ204082 719 bp mRNA linear E UI-R-DN1-cmv-e-08-0-UI.S1 UI-R-DN1 Rattus norvegicus UI-R-DN1-cmv-e-08-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-r@mail.nih.gov
Life Technologies catalog #: 11548-013
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/Dbrp/image/image.html
Insert Length: 2146 Std Error: 0.00
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
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High quality sequence stop: 364.
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11548-01
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Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.72 kb. Life Technologies catalog #:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="NCI_CGAP_Pan1"
/tissue_type="adenocarcinoma"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:
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> 718 CTAAGCGCGTTGATGCTGCCTTGGTGCTGGGATGCGTACATCAGTCTGCCCAATCTGCTG 120 LeuThrAlaLeuMetLeuProTrpGlyCysAspValGlnGlySerLeuSerSerLeuLeu 139

659

140 LysHisLeuGluGluValProGlnLeuValLysLeuGlyLeuLysAsnTrpArgLeuThr 159

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    451 Eckstein Medical Research Building Iowa City, IA 52242, USA Tel: 319 335 8250 Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Program for Rat Gene Discovery and Mapping University of Iowa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Soares, MB
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BQ204082.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /lab_host="DH10B (Life Technologies)"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-DN1 library is a normalized Rat Distal Colon library (nRDC)
                                                                                                                                                                                                                                                 TAG_SEQ=GAAGTGCTCC"
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/db_xref="taxon:10116"
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Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                    Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com).
end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AQ112439 (CIT-HSP-2372C1.TR CIT-HSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 301 838 0200 Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1998)
Other_GSSs: CIT-HSP-2372C1.TF
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1 (bases 1 to 630)

Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and
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/clone="2372C1"
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                                                                                                                                                                                                                                    /cell_type="Sperm"
/note="Vector: pBe
                                                                                                                                                                                                                                                               /sex="Male"
                                                                                                                                                                                                                                                                              /clone_lib="CIT-HSP"
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Creation of genome-wide protein expression libraries using random activation of gene expression
Mat. Biotechnol. 19 (5), 440-445 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 476)

Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R., Cain,S., Leventhal,C., Thornton,M.Ramachandran,R., Whittington,J., Lerner, Costan, C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: scain@athersys.com
High quality sequence stop: 
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BG210375 476 bp mRNA linear EST 21-APR-2
RST29913 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
BG210375
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Tel: 216 431 9900
Fax: 216 361 9596
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107 g 149 t 1 others
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/db_xref="taxon:9606"
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                111 IleAspArgMetAsnValLeuGluGlnLeuThrAlaLeuMetLeuProTrpGlyCysAsp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-24. For BAC
Clones are derived from the mouse BAC library Pieter de Jong
Library availability, please contact Pieter de Jong
(pdejong@mail.cho.org). Clones may be purchased from BACPAC
Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC
page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 88 row: D column: 12
Seg primer: T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1999)
Contact: Shaying Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zhao, S., Nierman, W., Malek, J., Shatsman, S., A)
Tsegaye, G., Geer, K., Krol, M., Shvartsbeyn, A.,
Russell, D., de Jong, P. and Fraser, C.M.
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                                                                                                                                                                                                                                                                                        /cell_type="Spleen/Brain"
/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
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/note="Vector pTARBAC1 cloning vector at the library was cloned in the pTARBAC1 cloning vector at the BamH1 sites using MboI partially digested male C57BL/6J
                                                                                                                                                                                                                                                                             DNA
                                                                                                                                                                                                                                                                                 BamH1 sites
DNA."
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/clone="RPCI-24-88D12"
/clone_lib="RPCI-24"
                                                                                                                                                                                                                                                                                                                                                                              /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hinxton, Cambridgeshire, CB10
Email: trop@sanger.ac.uk
Sanger xenopus tropicalis EST
TROPICALIS_SEQUENCE_ID: TNeu00
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This sequence is from a Xenopus Gene Collection (XGC) library constructed by Aaron M. Zorn.
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/dev_stage="neurula"
/dev_stage="neurula"
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                          uLeuIleAspArgMetAsnVal-----LeuGluGlnLeuThrAlaLeuMetLeuProTr 127
TTTGATTCCAGCTACCAACCTGACTCATCTGGATGCAATAATGACACTTTTGCTGCCTGG
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Amphibia; Batrachia; Anura;
Xenopodinae; Xenopus
1 (bases 1 to 577)
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BJ037401.1 GI:17420442
EST.
African clawed frog.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
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were oligo-dT primed and directionally cloned. Staging
according to Nieuwkoop and Faber. Library is subtracted
and was constructed by N. Garrett and A.M. Zorn,
(Wellcome/CRC Institute)."
107 c 114 g 179 t 1 others
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Batrachia; Anura; Mesobatrachia; Pipoidea;
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ProTrpGlyCysAspValGlnGlySerLeuSerSerLeuLeuLysHisLeuGluGluVal 145
                                    TCAGTAGAAGAACTGGCTGCCAACTTGACTCATCTTGATGCAATAAGGACACTTATGCTG
                                                                     AlaLeuHisGluLeuIleAspArgMetAsnValLeuGluGlnLeuThrAlaLeuMetLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sanger Centre
Hinxton, Cambridgeshire, CBIO 154, un
Email: tropésanger.ac.uk
Sanger Xenopus tropicalis EST project
Sanger Xenopus tropicalis TNeu037j15.sp6
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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AL657756
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                                                                                                                                                                                                                                                                                                /clone="TNeu037]15"
/clone_lib="XGC-neurula"
/clone_lib="XGC-neurula"
/dev_stage="neurula"
/lab_host="Socherichia coli DH10B"
/lab_host="Socherichia coli DH10B"
/note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
was oligo dT primed from 5ug of poly A+ RNA from neurula.
EcoRI-NotI cut cDNA was then ligated into pCS107 with
EcoRI at the 5' end and NotI at the 3' end."
156 c 128 g 209 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Silurana tropicalis"
/db_xref="taxon:8364"
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                      Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Quackenbush, J., Schriml, L.M., Staubli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Baldarelli, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C., Carninci, P., Ge Bonaldo, M.F., Brownstein, M.J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D.A., Kamiya, M., Lee, N.H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Brown, B., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Brown, R., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Brown, R., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Brown, R., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Brown, R., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Brown, R., Brown, R., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Brown, R., Marchionni, R., Ma
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1913 bp mRNA linear HTC 19-0 MUS musculus adult male testis cDNA, RIKEN full-length enrical library, clone:4933411P06:maternal effect gene, full insert
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                                                                                                                                                                                                                                                                                                                                                      Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S., Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I., Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R., Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T., Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T.,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Sakamoto, N.,
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                             /protein_id="BAB30427.1"
/db_xref="GI:12855703"
                                                                                                                                         putative"
                                                                                                                                                                              maternal effect
                                                                                                                                                                                                                evidence: ISS
                                                                                                                                                                                                                                                                           /gene="Mater"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="testis"
/clone_lib="RIKEN_full-length enriched mouse cDNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="FANTOM_DB:4933411P06"
/db_xref="MGD:MGI:1903594"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /strain="C57BL,
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/clone="4933411P06"
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                                                                                                        /codon_start=1
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DE 5 (bases 1 to 1913)

Adachi, J., Alzawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Arakawa, T., Baldarelli, R., Bono, H., Brownstein, M., Bult, C., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hill, D., Hiramoto, K., Hiraoka, T., Hori, F., Hume, D., Imotani, K., Ishil, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Mjyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Quackenbush, J., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Sohriml, L., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Tanaka, T., Fejima, Y., Toya, T., Yamamura, T., Yamanaka, I., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and
prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 10.0. Second strand cDNA was prepared with the primer adapter of sequence [5]
                                                                                                                                                                                                                                                     cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riker Genomic Sciences Center and Genome Excience Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGAGAGAGGAGCACCAAGAGCTCTTTTTTTTTTTTTTYN 3'], CDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H., Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L., Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S. and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gscriken.go.jp, URL:http://genome-gscriken.go.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fax:81-45-503-9216)
Please visit our web site (http://genome.gsc.riken.go.jp/) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (10-JUL-2000) Yoshihide Hayashizaki, The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Functional annotation of a full-length mouse cDNA collection Nature 409 (6821), 685-690 (2001)
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                               AAGTTGAAGCTGTGCTCTGCGTTCCAA 1460
                                                             TrpLeuAlaPheMetGlyValPheGlu 201
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                                                                                                                                                                                                                                                                                                                               41 SerAspIleGlyGlu---GlyMetAspTyrIleValLysSerLeuSerSerGluProCys 59
GlnLeuThrAlaLeuMetLeuProTrpGlyCysAspValGlnGlySerLeuSerSerLeu
                                         GGGGATGCGGGCCTGCAGCTGCTCTGCGAAGGACTCCTGGACCCCCAGTGCCGCCTGGAA
                                                                                                                                                    AlaGlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeu
                                                                                                                                                                                                        AAGATCCAGAAGCTGAGCCTCCAGAACTGCTGCCTGACGGGGGCCCGGCTGCGGGGTCCTG
                                                                                                                                                                                                                                             AspLeuGluGluIleGlnLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Scores:
                                                                           GluLysAspGlyAsnGluAlaLeuHisGlu---LeuIleAspArgMetAsnValLeuGlu 118
                                                                                                                        TCCAGCACACTACGCACCCTGCCACCCTGCAGGAGCTGCACCTCAGCGACAACCTCTTG
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Plate: LLCMI619 row: i column:
High quality sequence stop: 802.
Location/Qualifiers
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Tissue Procurement: Louis M. Staudt,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mRNA sequence.
BG684008
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National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelo
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
1 (bases 1 to 805)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BG684008
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CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
DNA Sequencing by: MCC clone distribution information can be
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Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1 8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II R (Life Technologies). Note: this is a NH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="IMAGE:4763594"
/clone_lib="NIH_MGC_48"
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/db_xref="taxon:9606"
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                              AATAATTCAATTGAGGATAAGGGTATGATGGTTTTGGGTGAATATTTAAAGGTTACACCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center For Genetic Resource Information
National Institute of Genetics
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel:
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EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Urushihara, H.,
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1 (bases 1 to 619)
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length cDNA of Dictyostelium discoideum at the culmination
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Location/Qualifiers
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/clone="ddc18j17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Dictyostelium/strain="AX4"
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59 c 108 g 222 t
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Result
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-Q=/Cgn2_1/USPTO_spool/US99697089/runat_29012003_092754_19735/app_query.fasta_1.981
-Q=/Cgn2_1/USPTO_spool/US99697089/runat_29012003_092754_19735/app_query.fasta_1.981
-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=p2n.rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=bitssum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US99697089 =GGGN_1_1_37_erunat_29012003_092754_19735 -NCPU=6 -TCPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XOAPOP=10 -XGAPEXT=0.5 -FGAPEXT=7
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1: /cgn2_6/ptodata/;

2: /cgn2_6/ptodata/;

3: /cgn2_6/ptodata/;

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6: /cgn2_6/ptodata/;
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/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/BcTUS_COMB.seq:*
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US-08-910-731-7

US-08-910-731-7

US-08-910-731-7

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                                                                                                                                          Sequence
263, Appli
3, Appli
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7, Appli
1, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 1
US-09-221-017B-263
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 26
Patent No.
                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION: APPLICANT: ROSS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               \frac{1}{4}
                                                                                                                                                                                                                              MEDIUM TYPE:
COMPUTER: IB
                                                                                                                                                                                                                                                                                            STATE: CA
                                                                                                                                                                                                                                                                                                        CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                    STREET:
                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                               263, Application US/09221017B
o. 6444799
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| 85.5 | ന | 86 | 86 | 86 | 86 | 86 | 86 | 86 | 86 | 86 | 86 | 7. | 87.5 | 88 | 8 | 88.5 | 9. | 90 | 90 | 90 | 91 | 91 | 91 | 91.5 | 97 | 97 | 97 | 97 | 97 | 97 | 97 | 97 |
|-----------------|-----------------|----------------|-----------------|-----------------|-----------------|------------|-----------------|-----------------|-----------------|-----------------|----------------|-------------------|------------|--------------|------------|-------------------|---------------|----------------|-------------|---------------|-------------------|------------|-----------|---------------|--------------|-------------|-----|------------|-------------|-------------|------------|------------------|
| | 8.2 | • | | ٠ | ٠ | ٠ | ٠ | ٠ | ٠ | | | ٠ | ٠ | | | • | | | • | ٠ | | | | | • | | • | • | • | 9.3 | | 9.3 |
| 2582 | 5785 | 78 | 78 | 94 | 94 | 94 | 94 | 62 | 62 | 62 | 62 | 47 | 57 | 84 | 14 | 14 | 29 | 80 | 80 | 8 | 4758 | 75 | 75 | 633 | 30 | 30 | 38 | 38 | 38 | 85 | 2859 | 85 |
| 1 | 4 | 4 | ω | 4 | 4 | 4 | ω | 4 | 4 | ω | w | 4 | 4 | ω | 4 | 4 | w | 4 | 4 | 4 | 4 | 4 | w | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 |
| US-08-514-014-3 | -08-488-237A-22 | -08-686-968C-2 | -08-480-640A-22 | -08-375-992A-18 | -08-488-237A-18 | 86-968C-18 | -08-480-640A-18 | -08-375-992A-11 | -08-488-237A-11 | -08-295-8 | -08-480-640A-1 | -09-353-58 | 9-353-585- | -08-986-485- | -207-359B- | -09-245-2 | -09-188-930-2 | -09-207-359в-2 | 9-245-281-2 | -09-099-041A- | -09-54 | 9-540-245A | -09-191-6 | -09-385-982-2 | 9-207-359B-3 | 9-245-281-3 | 9B- | 9-245-281- | 9-099-041A- | -09-207-359 | 9-245-281- | US-09-099-041A-9 |
| 3, Ap | 1, Ap | (U | 221, Ap | equence 189, Ap | e 189, Ap | e 189 | equence 189, Ap | e 113, Ap | equence 113, Ap | equence 113, Ap | e 113, Ap | Sequence 1, Appli | e 4, Appl | e 1, Appl | 42, | Sequence 42, Appl | : 228, Ap | : 25, App | 25, App | 25, App | Sequence 1, Appli | e 1, Appl | e 1, Appl | 206, Ap | 38, App | 38, App | • | e 7, Appl | e 7, Appl | e 9, Appl | equence 9, | , Appl |

ALIGNMENTS

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APPLICATION NUMBER: PP1546
FILING DATE: 30-CAN-1998
PRIOR APPLICATION DATA:
APPLICATION UNMBER: PP2911
FILING DATE: 09-APR-1998
PRIOR APPLICATION DATA:
APPLICATION UMBER: PCT/AU98/01023
FILING DATE: 10-DEC-1998
                                                                                                                                                                              APPLICATION NUMBER: PP1182
FILING DATE: 31-DEC-1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: Windows SOFTWARE: FastSEQ for Windows CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                             CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 94304-1018
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: ROSS, Bruce C.
TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF NUMBER OF SEQUENCES: 1120
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09 FILING DATE: 23-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: MORRISON & FOERSTER STREET: 755 PAGE MILL ROAD
                                                                                                                                                                                                                                                                                                                                                                                                       3: Diskette
IBM Compatible
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ATTORNEY/AGENT INFORMATION

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-221-017B-263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 8722 base pairs
 2806
                                                           2755
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                                                                                                              2695 CGTCTCACGTCCTTAGCAACGCTTGAACTATCGGGTAACCAAATCCGTAAGCTGGAGGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: 650-813-5600
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                                                                                      117
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ANTI-SENSE: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX:
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                                                                                                                                              AlaLeuHisGluLeu----
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                                                           CTGGAACGTCTCACGTCCTTAGCAACG---
                                                                                 LeuGluGlnLeuThrAlaLeuMetLeuProTrpGlyCysAspValGlnGlySerLeuSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTGGAACGTCTCACTTCGTTAACAAAGCTTCGTCTAAGAAGTAACCAGATCAGTAAACTA
AGTAAGCTAGAGGGTCTGGAACGTCTCTTCGTTAACAAAGCTTCGTCTAAGAAGTAAC
                         SerLeuLeuLysHisLeuGluGluValProGlnLeuValLysLeuGlyLeuLysAsnTrp 156
                                                                                                                                                                         ACTTCGTTAACAAAGCTTCGTCTAAGAAGTAACCAAATCAGTAAGCTAGAGGGTCTGGAA
                                                                                                                                                                                                                                                           LeuSerIleLeuAspLeuSerGluAsnTyrLeuGluLys----------
                                                                                                                                                                                                                                                                                                                     CysCysLeuSerAlaAsnAlaValLysIleLeuAlaGlnAsnLeuHisAsnLeuValLys
                                                                                                                                                                                                                                                                                                                                                                             IleValLysSerLeuSerSerGluProCysAspLeuGluGluIle---GlnLeuValSer 68
                                                                                                                                                                                                                                 TTAGCAACGCTTGAACTATCGGGTAACCAAATCCGTAAGCTAGAGGGTCTGGAACGTCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UNKNOWN
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42.92%
23.61%
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Indels:
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Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
                                                      ----CTTGAACTGTCGGGTAACCAAATC
                                                                                                                                           --IleAspArgMetAsnVal 116
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72
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β δ

196 AACGAGCTGGGCGATGTCGGCGTGCATTGCGTGCTCCAGGGCCTGCAGACCCCCTCCTGC 255

41 SerAspIleGlyGlu----GlyMetAspTyrIleValLysSerLeuSerSerGluProCys 59

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US-09-697-089-2_COPY_762_965 (1-204) x US-08-910-731-5 (1-1386)
                                              Best Local Similarity:
Query Match:
                                                                                               Score:
                                                                                                               Pred.
                                                                                                                            Alignment Scores:
                                                                                                                                                         ; MOLECULE TYPE: US-08-910-731-5
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US-08-910-731-5
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                                                                             Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5, Applicati
Patent No. 5932440
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                 TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 08/795,395
FILING DATE: 04-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/794,546
FILING DATE: 03-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., N.W., SUITE 600
                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/0:
FILING DATE: 16-AUG-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Rel CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2902
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                                                                                                              No . .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2866 CAGATCAGTAAACTAGAG--
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                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                       TYPE:
                                                                                                                                                                                                                                                                                                TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE: (Here
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                    LENGTH:
                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
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VENTION. .-
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                              Mismatches:
Indels:
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                                                                             Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/024,057
FILING DATE: 16-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: ESMOND, ROBERT W.
                                                                                                                                                   PRIOR APPLICATION NUMBER: 08/795,333

FILING DATE: 04-FEB-1997

PRIOR APPLICATION DATA:

PRIOR APPLICATION NUMBER: 08/794,546
              TELECOMMUNICATION INFORMATION: TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Mammalian Ribonuclease NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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                                           REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 0942.3440003
                                                                                                                                          APPLICATION NUMBER: 08/7 FILING DATE: 03-FEB-1997
                                                                                                                                                                                                                                             FILING DATE:
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                                                                                                                                                                                                                                                           APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                       PatentIn Release #1.0,
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                                                                    ROBERT W.
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Sequence 3, Application US/08795395
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Best Local Similarity:
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856 CTAGCTGGCAATGAGCTGAAGGATGAGGGT
                                  183 LeuAlaGlyAsnArgValSerSerAspGly
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GENERAL INFORMATION
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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NAME: ESMOND, ROBERT W.
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 60/024,057
FILING DATE: 16-AUG-1996
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AsnLeuH1sAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeuGluLys
                                          GAGAAGCTTCAGTTGGAATACTGTAACCTCACAGCTACCAGCTGCGCAGCCCCTGGCCTCA
                                                                                                                                 AspIleGlyGluGlyMetAspTyrIleValLysSerLeuSerSerGluProCysAspLeu 61
                                                                                                                                                                       GATGTGCTGCGCTTTTGTCTACCCTGCGTGAACTACATCTCAATGACAACCCTCTGGGG
                                                                         GluGluIleGlnLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeuAlaGln 81
                                                                                                                                                                                                   GluGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHis-----LeuSer 41
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20005-3934
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SYSTEM: PC-DOS/MS-DOS
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US-08-910-731-1
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               TELEFAX: 202-371-2540 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                         APPLICATION NUMBER: 08/7 FILING DATE: 04-FEB-1997 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IHM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                               TELECOMMUNICATION INFORMATION: TELEPHONE: 202-371-2600
                                                                                                                           FILING DATE: 16-AUG-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Rel CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: CHATTERJEE, DEB K. APPLICANT: SHANDILYA, HARINI
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Mammalian NUMBER OF SEQUENCES: 16
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                                                                                              NAME: ESMOND, ROBERT W
REGISTRATION NUMBER: 3:
                                                                                                                                                                                              APPLICATION NUMBER: 08/7 FILING DATE: 03-FEB-1997
                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
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Sequence 7, Application US/08910731
Patent No. 5932440
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: CHATTERJEE, DEB K.
APPLICANT: SHANDILYA, HARINI
TITLE OF INVENTION: Mammalian Ribonuclease
NUMBER OF SEQUENCES: 16
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LOCATION:
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STRANDEDNESS: both
TOPOLOGY: both
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Matches:
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Indels:
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                       Inhibitors
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                       Use
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 202-371-2540 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/794,546
FILING DATE: 03-FEB-1997
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REFERENCE/DOCKET NUMBER: 09
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 16-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: ESMOND, ROBERT W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 1371 base pairs
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APPLICATION NUMBER: 08/7
FILING DATE: 04-FEB-1997
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ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX
STREET: 1100 NEW YORK AVE., N.W., SUITE 600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/024,057 FILING DATE: 16-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/910,731 FILING DATE: (Herewith)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 1100 NEW CITY: WASHINGTON
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                      9 MetAspAsnIleLysMetAsnGluGluAspAlaIleLysLeuAlaGluGlyLeuLys---
GluAlaLeuHisGlu---LeuIleAspArgMetAsnValLeuGluGlnLeuThr-----
                                                     TCCCTGCCCACGCTGCGGGAGCTGCATCTCAGCGACCAACCCACTGGGGGACGCCGGCCTG
                                                                                                                             AGCCTGCAGAACTGCTCCCTGACCGAGGCGGGCTGCGGGGTCCTGCCCAGCACGCTGCGC
                                                                                                                                                                                                                                                                                                                                                   CTCGACGACTGCGGCCTCACGGAGGAGCACTGCAAGGACATCGGTTCTGCCCTCCGGGCC
                                                                                                                                                              GlnLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeuAlaGlnAsnLeuHis
                                                                                                                                                                                                    GCCGGCGTGCACCTGGTGCTGCAGGGCCTGCAGAGCCCCACCTGCAAGATCCAGAAGCTC
                                                                                                                                                                                                                                      ---GlyMetAspTyrIleValLysSerLeuSerSerGluProCysAspLeuGluGluIle
                                                                                                                                                                                                                                                                           AACCCCTCCCTGACCGAGCTCTGCCTC-
                                                                                                                                                                                                                                                                                                             -----AsnLeuLysLysMetCysLeuPheHisLeuThrHisLeuSerAspIleGlyGlu 45
                                                                                         AsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeuGluLysAspGlyAsn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IBM PC compatible SYSTEM: PC-DOS/MS-DOS
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10.66%
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Matches:
Conservative:
Mismatches:
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   Score:
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                                                                        us-08-795-395-1
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US-08-795-395-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/08795395 Patent No. 5965399
                                                                                                                                                                                                                         TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 09
TELECOMMUNICATION INFORMATION:
                                                                                                                           FEATURE:
                                                                                                                                           MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 16-AUG-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA:
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                                                                                                         NAME/KEY:
                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/0 FILING DATE: 04-FEB-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET:
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                                                                                                                                                                                            TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                LENGTH:
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Matches:
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                                                                                                                                                                                                                                                                                                     RESULT 8
US-09-221-017B-1118/c
US-09-221-017B-1118/c
; Sequence 1118, Application US/09221017B
; Patent No. 6444799
; Patent No. 6444799
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                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                        APPLICANT: ROSS, Bruce C.
TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF
NUMBER OF SEQUENCES: 1120
                SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              616
                                                                                                                                                                                                                                                                                                                                                                                                         670 CTGAGGGAGCTTGACCTGGGCAGCAACGGGCTGGGCGACGCGGGC
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                                               COMPUTER: IBM Compatible OPERATING SYSTEM: Windows
                                                                                                                       ZIP:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65 GlnLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeuAlaGlnAsnLeuHis
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                                                                                                                                         COUNTRY:
                                                                                                                                                          STATE:
                                                                                                                                                                        CITY: Palo Alto
                                                                                                                                                                                            STREET:
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 APPLICATION NUMBER:
                                                                                                                                                                                                            ADDRESSEE:
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                                                                                                                                           USA
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US/09/221,017B
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555 146 495 140 435 121 375 104 84

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PRIOR APPLICATION DATA:

APPLICATION NUMBER:

PRIOR APPLICATION DATA:

23-DEC-1998

APPLICATION NUMBER: CLASSIFICATION FILING DATE:

31-DEC-1997

PP1182

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Best Local Similarity:
Query Match:
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TELEX: 706141
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORIGINAL SOURCE:
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ATTORNEY/AGENT INFORMATION:
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143 GluGluValProGlnLeuValLysLeuGlyLeuLysAsnTrpArgLeuThrAspThrGlu 162
                                        308
                                                                                                                                                                              428
                                                                                                                                                                                                                                                    485
                                                                                                                                                                                                                                                                                                                    545 CAAATCAGTAAGCTAGAGGGTCTAGAACGTCTTACTTCGTTAACAAAACTTCGTCTAAGA 486
                                                                                                                                                                                                                                                                                                                                                                                        605 GAAAGCATGACTTGGCTTATTGATTTTCCTGCTCTAAAAAAAGCTTGATCTATCGTATAAC 546
                                                                                                                                                                                                                                                                                                                                                                                                              45 GluGlyMetAspTyrIleValLysSerLeuSerSerGluProCysAspLeuGluGluIle
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REGISTRATION NUMBER: 32,430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: PCT/AU98/01023 FILING DATE: 10-DEC-1998
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                                                                                                                                                                                                                                                                              AlaAsnAlaValLysIleLeuAlaGlnAsnLeuHisAsnLeuValLysLeuSerIleLeu 92
                                                                                                                                                                                                                                                  AGTAACCAAATCCGTAAACTA---GAGGGCCTGGATAGTCTCACCTCGCTAACAAAACTT 429
                                                                     LeuMetLeuProTrpGlyCysAspValGlnGlySerLeuSerSerLeuLeuLysHisLeu 142
                                                                                                        GAGCTTTATCTTTTGGATAACCAAATCAGTAAACTAGAGGGTCTGGAACGTCTCACGTCC
                                                                                                                                                                            TCTCTCTCCGATAACCAAATCAGTAAGCTAGAGGGTCTGGAACGTCTCACCTCGTTAGCG
                                                                                                                                                                                                             AspLeuSerGluAsnTyrLeuGluLys---AspGlyAsnGluAlaLeuHisGluLeu--- 110
                                    TTAACGGAGCTTTAT------CTGTCGGGTAACCAAATCAGTAAGCTAGAGGGTCTG
                                                                                                                                         -----IleAspArgMetAsnValLeuGluGlnLeuThrAla 122
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Matches:
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Best Local Similarity:
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US-09-180-439-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EARLIER APPLICATION NUMBER: PCT/GB97/01249
EARLIER FILING DATE: 1997-05-08
EARLIER APPLICATION NUMBER: GB 9609681.3
EARLIER FILING DATE: 1996-05-09
EARLIER APPLICATION NUMBER: GB 9619924.5
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CURRENT FILING DATE: 1998-12-06
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TYPE: DNA
ORGANISM: Lycopersicon esculentum
                                                                                                             2250
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                                      2310 CTTCACATTTTGTCG-----ATGTCATCTAATAGTTTCAGAGGAGAGCTCCCTTCATCT 2363
                                                                                                                                                                                  2190 AACGATCTCATTGGGGAAATTCCTTCATTTGTGTGCAATTTGACATCACTGGAAGTGTTG 224
                                                                                                                                                                                                                                                           2130 GGCTCTATTCCTGCTTCATTTGGCAATATGAGAAATCTGCAAACTCTGTTTCTCAGTGAT
                                                                                                                                                                                                                                                                                                                                  2073 TCATTGGGG---AATCTAAACAACTTGTCTAGGTTGTATCTTTACAATAATCAGCTTTCT 2129
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83 LeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeuGluLysAsp 102
                                                                                                                                                                                                                                                                                                                                                                  21 LysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHis-----
                                                                                                                                                                                                                                                                                                                                                                                                                            IleGlnLeuValSerCysCysLeuSerAlaAsnAlaValLys---IleLeuAlaGlnAsn 82
                                                                                                             TATATGTCGAGAAACAATTTGAAGGGAAAAGTTCCGCAATGTTTGGGTAATATCAGTGAC
                                                                                                                                                                                                                                                                                                                                                                                                         CTGAGTTCTCTTACTGAACTATTTTTTGGGTAATAACTCTCTTAATGGCTCTATTCCTGCT
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                                                                                                                                               -----ProCys-----AspLeuGluGlu 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hatzixanthis,
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; LENGTH: 3979
; TYPE: DNA
; ORGANISM: Lycopersicon
US-09-180-439-2
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                                                                                                                                                                                                                                                                                                                         SEQ ID NO 2
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                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Plant pathogen resistance FILE REFERENCE: 620 - 53
CURRENT APPLICATION NUMBER: US/09/180,439
CURRENT FILING DATE: 1998-12-06
EARLIER APPLICATION NUMBER: PCT/GB97/01249
EARLIER FILING DATE: 1997-05-08
                                                                                                                                                                                                                                                                                                                                                 EARLIER APPLICATION NUMBER: GB 9609681.3
EARLIER FILING DATE: 1996-05-09
EARLIER APPLICATION NUMBER: GB 9619924.5
EARLIER FILING DATE: 1996-09-24
NUMBER OF SEQ ID NOS: 10
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                             CTGAGTTCTCTTACTGAACTATTTTTGGGTAATAACTCTCTTAATGGCTCTATTCCTGCT 2072
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LysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHis....
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                                                                                                                                                                                                                                                                                          Sequence 7, Application Patent No. 6225532
                                                                          CURRENT APPLICATION NUMBER: US/09/180,439
CURRENT FILING DATE: 1998-12-06
EARLIER APPLICATION NUMBER: PCT/GB97/01249
EARLIER FILING DATE: 1997-05-08
EARLIER APPLICATION NUMBER: GB 9609681.3
EARLIER FILING DATE: 1996-05-09
                                                                                                                                                                            TITLE OF INVENTION: Plant pathogen resistance FILE REFERENCE: 620 - 53
                                                                                                                                                                                                          APPLICANT: Jones, David A APPLICANT: Jones, Jonathan DG
                SOFTWARE: PatentIn
                            EARLIER FILING DATE: 1996-09-24
NUMBER OF SEQ ID NOS: 10
                                                            EARLIER APPLICATION NUMBER: GB 9619924.5
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: 303/863-9700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: KOVATÍK, JOSEPh E.
REGISTRATION NUMBER: 33,005
REFERENCE/DOCKET NUMBER: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
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 403
                                                             355
                                                                                                                                                                                        238
                                                                                                                                                                                                                                                     184 CTTAAAGATTTAACTAAGTTAGTT-----GATATTTTGATGAATAATAATCAAATAGCA 237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: PCT FILING DATE: 18 AUGUST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: Colorado COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                    CAGCAATTATCTTTTGGTAATCAAGTGACAGATTTAAAACCATTAGCT-------
                             GlnLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeuAlaGlnAsnLeuHis 84
                                                             AGTAACACGATTAGTGATATTAGTGCGCTTTCAGGT---
                                                                                                                           CAGATAACAGATATAGACCCGCTTAAAAATCTAACAAATTTAAATCGGCTAGAACTATCT 354
                                                                                                                                                                                        GATATAACTCCGCTAGCT---AATTTGACGAATCTAACTGGTTTGACTTTGTTCAACAAT
                                                                                                                                                                                                         AspAlaIleLysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPhe-----
                                                                                         MetAspTyrIle-----ValLysSerLeuSerSerGluProCysAspLeuGluGluIle 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleic acid
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1700 Lincoln Street, 35th Floor
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Sawyer, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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26.19%
9.46%
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IST 1995
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                                                                                                                                          --HisLeuThrHisLeuSerAspIleGlyGluGly 46 :::||||||:::|||:::
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                                                             -TTAACTAATCTA
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| Qy 129 | Qy 113 Db 2185 | Qy 93 Db 2125 | Qy 83 Db 2065 | Qy 65 Db 2005 | us-09-697- | Alignment: Pred. No.: Score: Score: Percent Sin Best Local Query Matcl DB: | Db 670 TTAK RESULT 13 US-09-099-041) Sequence 9, Patent NO. GENERAL INFO APPLICANT: TITLE OF II TITLE OF II TITLE OF II CURRENT APPL CURRENT FILI PRIOR FILI PRIOR FILI PRIOR FILI PRIOR FILI SEQ ID NO 9 SEQ ID NO 9 INVESTIGNE TYPE: DNA ORGANISM: US-09-099-0411 | | Qy 161 Db 619 | Qy 145 Db 559 | Qy 125 Db 526 | Oy 105 Db 490 | Db 451 |
|--------------------------------|---|--|---|---|-----------------|--|---|--|--|--|--|--|---|
| CysAspValG | ArgMetAsnValLeu- ::: CGCCTCACTGTTCTCA | AspLeuSerGluAsn GACCTAGACAACAAC | TCGGCCGACT | GlnLeuValS | 089-2_COPY_7 | ment Scores: . No.: s: ont Similarity: Local Similarity: Match: | SSULT 13 Sequence 9, Application US/0 Patent NO. 6340576 GENERAL INFORMATION: APPLICANT: BETTIN, John TITLE OF INVENTION: NOVEL M TITLE OF INVENTION: PROTEI FILE REFERENCE: 07334-07500 CURRENT FILING DATE: 1998-02- RIOR APPLICATION NUMBER: 0 PRIOR FILING DATE: 1998-02- NUMBER OF SEQ ID NOS: 37 SOFTWARE: FastSEQ for Windo SEQ ID NO 9 LENGTH: 2859 TYPE: DM: ORGANISM: Homo sapiens -09-099-041A-9 | LeuAsnLeuA ::: | ThrGluIleA::::::: AACCAGTTAA | ValProGlnL ::: ATAAGTGATA | LeuProTrpG | GluAlaLeuH | AATTTAACAA |
| GlnGlySerLeu | alLeuGluGlnLeuThrAlaLeuMetLeuProTrpGly TTCTCAGACTCAGCGTAAACCAGATCACT | pLeuSerGluAsnTyrLeuGluLysAspGlyAsnGluAlaLeuHisGluLeuIleAs | | InLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeuAlaGlnAsn ::: | _762_965 (1- | 0.0203 97.00 35.00% y: 23.33% y: 27.3 | O TTAGATTTAGCAAATAACCAAATTAG 3 9-041A-9 19-041A-9 10Ce 9, Application US/0909904 NO. 6340576 L INFORMATION: CANT: Bertin, John CANT: Bertin, John COF INVENTION: NOVEL MOLECUL OF INVENTION: PROTEIN FAMI REFERENCE: 07334-076001 REFERENCE: 07334-076001 REFERENCE: 07334-076001 REFERENCE: 10734-076001 REFERENCE: 1938-0-0-0-0-0-0-0-0-0-0-0-0-0-0-0-0-0-0-0 | LeuAsnLeuAlaGlyAsnArgValSerSer ::: ::::: ::: | ThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPheGlnGln :::::::: ;;;;;;;;;;;;;;;;;;;;;;;;;;;; | ValProGlnLeuValLysLeuGlyLeuLysAsnTrpArgLeuThrAsp ::: | LeuProTrpGlyCysAspValGlnGlySerLeuSerSerLeuLeuLysHisLeuGluGlu | lualaLeuHisGluLeuIleAspArgMetAsnValLeuGluGlnLeuThrAl::: ::::: ::: AAGGTGTCAGATATTAGTGTTCTGGCTAAATTAACC | AATTTAACAACACTAGAACGACTAGATATTTCAAGTAAT |
| erLeuSerSerLeuLeuLysHisLeuGluG | GluGl AGCGTAAACCA | TyrLeuGluLysAspGlyAsnGluAlaLeuHisGluLeuIleAsp AATCTCAACGACTACGGCGTGCGGGAGCTGCAGCCCTGCTTCAGC | TCCTTCGTCCT | SerAlaAsnAl TGCGCCAACTA | 204) x | Len Mat Con Mis Ind Gap | TTAGTAAT : 99041A 99041A COLUES OF FAMILY AND S/09/099, 17 19,942 Version | | AlaPhePheGl ACATTGGCGAG | Gly GGGATTTTAAC | GlnGlySerLe ::: AATTT | AspargMetas ::::: TCAGATATTAG | TAGATATTTC |
| uLysHisLeu(| nLeuThrAlaI ::: GATCACT | yAsnGluAlaI CGTGCGGGAGO | LeuHisAsnLeuValLysLeuSer ::: TGCATCACTTCCCCAAGCGGCTG | aValLysIleI ::: ::: CCTCAAGCTG | US-09-099-041A- | Length: Matches: Conservative: Mismatches: Indels: Gaps: | 999 THE CARD- USES THE | 190 | yLysAsnProl | LeuLysi AAATTTGGACO | SerLeuSerSerLeuLeuLysHisLeuGluGlu | nValleuGlu | AAGTAAT |
| luValp | LeuMetLeuPr | LeuHisGluLe TGCAGCCCTG | ValLysLeuSe CCCAAGCGGCT | LeuAlaGlnAs - ACCTACTGCAA | A-9 (1-2859 | 2859 655 521 | RELATED | | LeuLysAsnPheGlnGln TTAACAAACCTTACAGAT | LeuLysasnTrpArgLeuThras TTGGACGAATTATCCTTAAATGG | LeuLysHisLe ::: ATCGCTACTAA | GlnLeuThrAl ::: AAATTAACC | 1 |
| roGlnLeu | | G B | erIleLeu GGCCCTA | CGCCTGC | 3 | | | | neGlnGln TACAGAT | euThrAsp AAATGGT | euGluGlu ::: CAACCAA | aLeuMet | |
| 148 | 128 2223 | 112 2184 | 92 2124 | 82 2064 | | | | | 180 669 | 160 618 | 144 558 | 124 525 | 489 |

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GENERAL INFORMATION:
APPLICANT: Bertin, John
ITILE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY
ITILE OF INVENTION: AND USES THEREOF
ITILE OF INVENTION: AND USES THEREOF
ITILE OF INVENTION INDUSTRIES
CURRENT APPLICATION NUMBER: US/09/245,281
CURRENT FILING DATE: 1998-02-05
EARLIER APPLICATION NUMBER: US 09/207,359
EARLIER FILING DATE: 1998-12-08
EARLIER FILING DATE: 1998-12-08
EARLIER APPLICATION NUMBER: US 09/09,041
EARLIER APPLICATION NUMBER: US 09/09,041
EARLIER FILING DATE: 1998-06-17
EARLIER FILING DATE: 1998-06-17
EARLIER FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 44
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; LENGTH: 2859
; TYPE: DNA
; ORGANISM: HOMO s
US-09-245-281-9
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Best Local Similarity:
Query Match:
DB:
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US-09-245-281-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: FastSEQ
SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 9, Application US/09245281 Patent No. 6369196
    2224
                                                                                2185
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                                                                                                                                                                                                                                                                                                                      2005 CAGCTGGCGGCCAGGGGCATCTGCGCCAACTACCTCAAGCTGACCTACTGCAACGCCTGC 2064
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                                     CysaspValGlnGlySerLeuSerSerLeuLeuLysHisLeuGluGluValProGlnLeu 148
                                                                                                                    ArgMetAsnValLeu-----
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                                                                                CGCCTCACTGTTCTCAGACTCAGCGTAAACCAGATCACT--
                                                                                                                                                                                              AspLeuSerGluAsnTyrLeuGluLysAspGlyAsnGluAlaLeuHisGluLeuTleAsp 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LeuAlaGlyAsnArgValSerSerAspGlyTrpLeuAlaPheMetGlyValPheGluAsn
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-----GACGGTGGGGTAAAGGTGCTAAGCGAAGAGCTGACCAAATACAAAATTGTG 2274
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Matches:
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| Qy 129 CysAspValGlnGlySerLeuSerSerLeuLeuLysHisLeuGluGluValProGlnLeu 148 |
| Qy 113 ArgMetAsnValLeuGluGlnLeuThrAlaLeuMetLeuProTrpGly 128 |
| Qy 93 ASPLeuSerGluAsnTyrLeuGluLysAspGlyAsnGluAlaLeuHisGluLeuIleAsp 112 |
| Qy 83 |
| Qy 65 GlnLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeuAlaGlnAsn 82 |
| US-09-697-089-2_COPY_762_965 (1-204) x US-09-207-359B-9 (1-2859) |
| Alignment Scores: 0.0203 Length: 2859 Pred. No.: 97.00 Matches: 42 Percent Similarity: 35.00% Conservative: 21 Best Local Similarity: 23.33% Mismatches: 65 Query Match: 9.27% Indels: 52 DB: 4 Gaps: 5 |
| Qy 169 Phe |
| Qy 149 VallysLeuGlyLeuLysAsnTrpArgLeuThrAspThrGluIleArgIleLeuGlyAla 168 |

Search completed: January 31, 2003, 15:16:46 Job time: 51.1802 secs

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Title:
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-DB-Published_Applications_NA -QFMT-fastap -SUFFIX-p2n.rnpb -MINMATCH-0.1
-LOOPCL-0 -LOOPEXT-0 -UNITS-bits -STAFT=1 -END--1 -MATRIX-blosum62
-TRANS-human40.cdi -LIST-45 -DOCALIGN=200 -THR_SCORE-pct -THR_MAX=100
-THR_MIN-0 -ALIGN-15 -MODE-LOCAL -OUTFMT-pto -NORM-ext -HEAPSIZE-500 -MINLEN-0
-MAXIEN-2000000000 -USER-US09697089_eCGN 1_148 @runat_29012003_092755_19800
-NCPU-6 -ICPU-3 -NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES-0 -WAIT -LONGLOG
-DEV_TIMEOUT-120 -WARN_TIMEOUT-30 -THREADS-1 -XOAPDAT-0.5 -FGAPOP-6
-FGAPEXT-7 -YGAPOP-10 -YGAPEXT-0.5 -DELOP-6 -DELEXT-7
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Sequence 98, Appl
Sequence 3, Appli
Sequence 1, Appli
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ALIGNMENTS

US-09-864-921-181

181,

Application US/09864921

Patent No. US20020176853A1 GENERAL INFORMATION:

APPLICANT: Reed, APPLICANT: Pio, APPLICANT: Godzi

John C. Frederick F.

```
APPLICANT: Stehlik, Christian
APPLICANT: Damiano, Jason S.
APPLICANT: Lee, Sug-Hyung
APPLICANT: Lee, Sug-Hyung
APPLICANT: Oliveira, Vasco A.
APPLICANT: Oliveira, Vasco A.
APPLICANT: Hayashi, Hideki
APPLICANT: Pawlowski, Krzysztof
TITLE OF INVENTION: No. US20020176853Alel Card Domain Containing
TITLE OF INVENTION: Polypeptides, Encoding Nucleic Acids, and Methods of Use
FILE REFERENCE: P-LJ 4752
CURRENT APPLICATION NUMBER: US/09/864,921
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 09/579,240
PRIOR FILING DATE: 2000-05-24
PRIOR FILING DATE: 2000-05-24
PRIOR APPLICATION NUMBER: US 09/686,347
PRIOR APPLICATION NUMBER: US 09/686,347
PRIOR APPLICATION NUMBER: US 09/686,347
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PRIOR APPLICATION NUMBER: US 09/686,347
PRIOR APPLICATION NUMBER: US 09/686,347
PRIOR APPLICATION NUMBER: US 09/686,347
PRIOR APPLICATION NUMBER: US 09/686,347
PRIOR APPLICATION NUMBER: US 09/579,980
PRIOR FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 195
SOFTWARE: FastSEQ for Windows Version 4.0
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TYPE: DNA
ORGANISM: HOMO :
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...
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APPLICANT: Reed, Jr
APPLICANT: Pio, F
APPLICANT: Godzik
APPLICANT: Stehlil
APPLICANT: Damiano
APPLICANT: Lee, S
                                             Sequence 98, Application U Patent No. US20020176853A1 GENERAL INFORMATION:
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       Reed, John C.
Pio, Frederick |
Godzik, Adam
Stehlik, Christ
Damiano, Jason
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APPLICANT: Oliveira, Vasco A.
APPLICANT: Hayashi, Hideki
APPLICANT: Hayashi, Hideki
APPLICANT: Pawlowski, Krzysztof
TITLE OF INVENTION: No. US20020176853Alel Card Domain Containing
TITLE OF INVENTION: No. US20020176853Alel Card Domain Containing
TITLE OF INVENTION: Polypeptides, Encoding Nucleic Acids, and Metho
FILE REFERENCE: P-LJ 4752
CURRENT APPLICATION NUMBER: US/09/864,921
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 09/579,240
PRIOR FILING DATE: 2000-05-24
PRIOR FILING DATE: 2000-10-10
PRIOR APPLICATION NUMBER: US 60/275,980
PRIOR APPLICATION NUMBER: US 60/275,980
PRIOR FILING DATE: 2001-03-14
NUMBER OF SEO ID NOS: 195
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; LOCATION: (277)...(1353)
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APPLICANT: Bertin, John
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES
FILE REFERENCE: 07334-329001
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PRIOR APPLICATION NUMBER: US 60/161,822
PRIOR FILING DATE: 1999-10-27
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 4.0
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CURRENT FILING DATE: 2001-08-29
PRIOR APPLICATION NUMBER: US 09/697,089
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US-09-841-739-1
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LENGTH: 3133
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PRIOR ETLING DATE: 2000-10-26
PRIOR APPLICATION NUMBER: US 60/161,822
PRIOR FILING DATE: 1999-10-27
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LOCATION: (277)...(3348)

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CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 09/579,240
PRIOR FILING DATE: 2000-05-24
PRIOR APPLICATION NUMBER: US 09/686,347
PRIOR APPLICATION NUMBER: US 09/686,347
PRIOR APPLICATION NUMBER: US 06/275,980
PRIOR FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 195
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TITLE OF INVENTION: NO. US20020176853Alel Card Domain Containing
TITLE OF INVENTION: Polypeptides, Encoding Nucleic Acids, and Methods
FILE REFERENCE: P-LJ 4752
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APPLICANT: Pio, Frederick F.
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ENGTH: 3396
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Oliveira, Vasco A.
Hayashi, Hideki
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US-09-841-739-6
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APPLICANT: Bertin, John
TITLE OF INVENTION: NOVEL MOLECULES OF THE
FILE REFERENCE: 07334-329001
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CURRENT FILING DATE: 2001-08-29
PRIOR APPLICATION NUMBER: US 09/697,089
PRIOR FILING DATE: 2000-10-26
PRIOR APPLICATION NUMBER: US 60/161,822
PRIOR FILING DATE: 1999-10-27
NUMBER OF SEQ ID NOS: 16
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ORGANISM: Homo
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CURRENT APPLICATION NUMBER: US/09/841,739
CURRENT FILING DATE: 2001-08-29
PRIOR APPLICATION NUMBER: US 09/697,089
PRIOR FILING DATE: 2000-10-26
PRIOR APPLICATION NUMBER: US 60/161,822
PRIOR FILING DATE: 1999-10-27
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 4
                                                                        Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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                                                                                                                                                                                                   ORGANISM: Homo FEATURE:
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                                                                                                                                                                                                                                                                                                                                 Sequence 12, Application US/09841739 Patent No. US20020034784A1
                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/841,739
CURRENT FILING DATE: 2001-08-29
PRIOR APPLICATION NUMBER: US 09/697,089
PRIOR FILING DATE: 2000-10-26
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TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES
FILE REFERENCE: 07334-329001
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PRIOR FILING DATE: 1999-10-27
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 4
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CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
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                          RENT FILING DATE: 2001-05-23

TOR APPLICATION NUMBER: US 60/180,312

FILING DATE: 2000-02-04

FOR APPLICATION NUMBER: US 60/207,456

FOR FILING DATE: 2000-05-26

FOR FILING DATE: 2000-08-03

FOR APPLICATION NUMBER: US 09/632,366

FOR FILING DATE: 2000-08-03

FOR APPLICATION NUMBER: US 60/236,359

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   FILING DATE: APPLICATION
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Chen, Wensheng
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Hanzel, David K.
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                                                    Sequence 20, Application US/09986224
Patent No. US20020150920A1
GENERAL INFOCMATION:
APPLICANT: Bertin, John
APPLICANT: Wang, Weiye
APPLICANT: Blatcher, Maria
TITLE OF INVENTION: NOVEL MOLECULES OF THE
FILE REFERENCE: 07334-33301
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ICR APPLICATION NUMBER: PCT/USO1/00662
ICR APPLICATION NUMBER: PCT/USO1/00661
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ICR APPLICATION NUMBER: PCT/USO1/00670
ICR APPLICATION NUMBER: US 00/234,687
ICR APPLICATION NUMBER: US 09/34,687
ICR APPLICATION NUMBER: US 09/34,687
ICR APPLICATION NUMBER: US 09/608,408
ICR FILING DATE: 2000-06-30
ICR APPLICATION NUMBER: US 09/774,203
ICR FILING DATE: 2001-01-29
ICR APPLICATION NUMBER: US 09/774,203
ICR FILING DATE: 2001-01-29
ICR APPLICATION NUMBER: US 09/774,203
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ER INFORMATION: EXPRESSED II
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APPLICATION NUMBER: PCT/US01/00669
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00665
FILING DATE: 2001-01-30
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APPLICATION
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N FETAL LIVER, SIGNAL = 1.2

N LUNG, SIGNAL = 1.2

IN BRAIN, SIGNAL = 1.2

IN HEART, SIGNAL = 1.2

IN HELLA, SIGNAL = 1.6

IN HELLA, SIGNAL = 1.6

IN HELLO, SIGNAL = 1.8

IN PLACENTA, SIGNAL = 1.8

IN PLACENTA, SIGNAL = 1.8

IN BONE MARROW, SIGNAL = 1.
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NUMBER OF SEQ ID NOS: 20
SOFTWARE: FastSEQ for Windows
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APPLICANT: Bertin, John
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CURRENT FILING DATE: 2001-10-22
PRIOR APPLICATION NUMBER: US 09/848,035
PRIOR FILING DATE: 2001-05-03
PRIOR APPLICATION NUMBER: US 60/201,464
PRIOR FILING DATE: 2000-05-03
NUMBER OF SEQ ID NOS: 20
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APPLICANT: Blatcher, Maria
TITLE OF INVENTION: NOVEL MOLECULES OF THE
FILE REFERENCE: 07334-333001
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SerSerLeuLysHisLeuGluGluValProGlnLeu---
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                                 LeuGlyLeuLysAsnTrpArgLeuThrAspThrGluIleArgIleLeuGlyAlaPhePhe
                                                                                                                                                                                                                 LeuThrAlaLeuMetLeuProTrpGlyCysAspValGln------GlySerLeu 135
                                                                                                                                                                                                                                                  AGAGACGAGGAGTCAAGTTCCTGTGAGGCCTTGGGTCGCCCAGAT-----GGTAAC 2550
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                                                                CAGGATGATGGAGTGAAGCTACTGTGTGAGGCTCTGAAACCACATCGTGCATTGCACACA
                                                                                                                          GCTAATGCCCTCAGCCATAATCATAATGTGAAAATCTTGGATTTGGGAGAAAATGATCTT
                                                                                                                                                                                      CTGCAGAGCCTGAATTTGTCA---GGTTGTTCTTTCACAAGAGAGGGGCTGTGGAGAGCTG
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Matches:
Conservative:
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Indels:
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; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1194
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US-09-938-842A-1194
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1194, Application US/09938842A Patent No. US20020160378A1 GENERAL INFORMATION:
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LENGTH: 1581
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PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
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APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF
TITLE OF INVENTION: SAME, AND METHODS OF USE
TILE REFERENCE: SCRIP1300-3
CURRENT EPPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
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PRIOR FILING DATE: 2000-08-24
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                                                                                      AlaValLysIleLeuAlaGlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeu 94
                                                                                                                                                                                                                                                                                                                                                                                                                                       SerGluProCysAspLeuGluGlu---IleGlnLeuValSerCysCysLeuSerAlaAsn
                                                                                                                                                                                                           GAGTCTATAGGAGATTTGCTAAACTTGGTCAACCTGAATCTTAGTGGAAACCAATTATCA
                                                                                                                                                                                                                                                                                                                                                                                   AlaGluGlyLeuLys----AsnLeuLysLysMetCysLeuPheHisLeu-------
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                                  SerGluAsnTyrLeuGluLys-----
                                                                                                                                                                                                                                                                                GGAGGGCTTATTTCTTTGACGAGGCTTGATTTGCATTCGAATAGAATTGGTCAGCTCCCT
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                                                                    AGCCTCTCTATTCTCCCTGAATCTATTGGTTCTCTCGTGAGCCTAAAGAAGCTCGATGTT
                                                                                                                                         TCTCTTCCATCGTCATTTAATAGATTGATACATCTTGAGGAACTTGATTTGAGCTCTAAC
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Matches:
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              PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-08
PRIOR FILING DATE: 1999-09-13
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CURRENT APPLICATION NUMBER: US/09/905,291A
CURRENT FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR FILING DATE: 2000-02-22
                                                                                                                                                                                                                                                                                                                 APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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FILING DATE: APPLICATION 1
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Stewart, Timothy A.
                                                                                                                                                                                                                                                                                                                                                                                                 Tumas, Daniel
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Mather, Jennie P.
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Hillan, Kenneth, J.
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Grimaldi, Christopher
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Eaton, Dan L.
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OR FILING DATE: 1999-11-30
OR APPLICATION NUMBER: PCT/US99/28564
OR FILING DATE: 1999-12-02
OR APPLICATION NUMBER: PCT/US99/28565
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OR APPLICATION NUMBER: PCT/US99/30095
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APPLICATION NUMBER: PCT/US99/28214
FILING DATE: 1999-11-29
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CURRENT APPLICATION NUMBER: US/10/066,500
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PRIOR APPLICATION NUMBER: 60/066840
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PRIOR FILING DATE: 1997-10-29
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PRIOR APPLICATION NUMBER: 60/063082
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                                     APPLICATION NUMBER: FILING DATE: 1998-08
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                                                                                            APPLICATION NUMBER: 60/095998
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P.Mickey Williams
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Mary A. Napier
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Ivar J. Kljavin
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David A. Botstein
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APPLICATION NUMBER: 6 FILING DATE: 1998-09-FILING DATE: 1998-09-1 APPLICATION NUMBER: 60 FILING DATE: 1998-09-1

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FILING DATE: 1998-10-28
APPLICATION NUMBER: 60/109304
FILING DATE: 1998-11-20
APPLICATION NUMBER: 60/125778

APPLICATION NUMBER: FILING DATE: 1998-09-24 APPLICATION NUMBER: 60/101922

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APPLICATION 1998-09-07-07-098/18924
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APPLICATION NUMBER: 09/886342
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APPLICATION NUMBER: PCT/US98/14552
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APPLICATION NUMBER: 09/767609
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FILING DATE: 2001-05-30
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                                                ---GGTATCGCCGAGGGC
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OR APPLICATION NUMBER: 09/136801
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APPLICATION NUMBER: 08/933821
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APPLICATION NUMBER: 08/960507
FILING DATE: 1997-10-29

APPLICATION NUMBER: 09/ FILING DATE: 1998-07-14

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APPLICATION NUMBER: 60/169495 FILING DATE: 1999-12-07 APPLICATION NUMBER: 08/918874

APPLICATION NUMBER: 60/149396 FILING DATE: 1999-08-17 APPLICATION NUMBER: 60/145698 FILING DATE: 1999-07-26

APPLICATION NUMBER: 60/ FILING DATE: 1999-07-20 APPLICATION NUMBER: 60/139695 FILING DATE: 1999-06-15 FILING DATE: 1999-03-23

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OR APPLICATION NUMBER: 09/380137

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APPLICATION NUMBER: 09/:
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R APPLICATION NUMBER: 09/254460

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R APPLICATION NUMBER: 09/284663

R FILING DATE: 1999-04-15

R FILING DATE: 1999-06-14

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CURRENT APPLICATION NUMBER: US/09/902,853
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US/09/665,350
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-07
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides
TITLE OF INVENTION: Acids Encoding the Same
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FILING DATE: 1999-07-28
APPLICATION NUMBER: PC7US99/20594
FILING DATE: 1999-09-08
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                                                APPLICATION NUMBER: PCT/US99/20944 FILING DATE: 1999-09-13
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Stewart, Timothy A.
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Hillan, Kenneth, J.
Kljavin, Ivar J.
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Grimaldi, Christopher J.
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Filvaroff, Ellen
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Eaton, Dan L.
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Botstein, David
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NUMBER: PCT/US99/21547
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: HOMO US-09-902-853-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR PPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 2000-01-05
PRIOR FILING DATE: 2000-01-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 27
LENGTH: 2479
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PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
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TYPE: DNA
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PRIOR FILING DATE: 1999-11-29
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                                                                                                                  119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 1999-09-15
                                                                                                                                                                                                                                 CCTTTGACAGCCTTCTCAAATCTGCGTAAGCTGGAACGGCTGGATATATCCAACAACCAA 1124
                                                                                                                                                                                                                                                                                                               GATCTCCCAGGTACGCATCTGATCAGGCTCTATTTGCAGGACAACCAGATAAACCACATT 1064
                                                                                                                                                                                                                                                                                                                                             AspLeuGluGluIleGlnLeuValSerCysCysLeuSerAlaAsnAlaValLys---Ile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IleLysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHis
                                                                           CAGCTCACTGCTCGGAATAACCCTTGGTTTTGTGACTGC-----AGTATTAAATGGGTC
                                                                                                                GlnLeuThrAlaLeuMetLeuProTrpGlyCysAspValGlnGlySerLeuSerSerLeu
                                                                                                                                                         CTGCGGATG------CTGACTCAAGGGGTTTTTGATAATCTCTCCAACCTGAAG
                                                                                                                                                                                    LeuGluLysAspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGlu 118
                                                                                                                                                                                                                                                                      LeuAlaGlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyr 98
                                                                                                                                                                                                                                                                                                                                                                                            CTCAAGGAA---
                                                                                                                                                                                                                                                                                                                                                                                                                               LeuSerAspIleGlyGluGlyMetAspTyrIleValLysSerLeuSerSerGluProCys 59
ACAGAATGGCTCAAATATATCCCT
                                    LeuLysHisLeuGluGluValPro
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Search completed: January 31, Job time: 61.4923 secs

2003, 18:05:20

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52_965.p2n.cappm
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Title:
Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPDP=10 -XGAPEXT=0.5 -FGAPDP=6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Scoring table:
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Maximum DB
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[cgn2_6/ptodata/2/pna/U]

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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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1 LKNLTKLIMDNIKMNEEDAI......GNRVSSDGWLAFMGVFENLK 204
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: /cgn2_6/ptodata/2/pna/US086_COMB.seq: *
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Copyright (c) 1993 - 2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /cgn2_6/ptodata/2/pna/US080_COMB.seq:*
/cgn2_6/ptodata/2/pna/US080_COMB.seq:*
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/cgn2_6/ptodata/2/pna/US07_COMB.seq:*
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/cgn2_6/ptodata/2/pna/US082_COMB.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /cgn2_6/ptodata/2/pna/PCTUS
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29: /cgn2_6/ptodata/2/pna/US097B_COMB.seq; * 31: /cgn2_6/ptodata/2/pna/US097C_COMB.seq; * 31: /cgn2_6/ptodata/2/pna/US098A_COMB.seq; * 32: /cgn2_6/ptodata/2/pna/US098A_COMB.seq; * 34: /cgn2_6/ptodata/2/pna/US098B_COMB.seq; * 35: /cgn2_6/ptodata/2/pna/US099B_COMB.seq; * 36: /cgn2_6/ptodata/2/pna/US099B_COMB.seq; * 37: /cgn2_6/ptodata/2/pna/US099B_COMB.seq; * 39: /cgn2_6/ptodata/2/pna/US099B_COMB.seq; * 39: /cgn2_6/ptodata/2/pna/US099B_COMB.seq; * 39: /cgn2_6/ptodata/2/pna/US099B_COMB.seq; * 40: /cgn2_6/ptodata/2/pna/US099B_COMB.seq; * 41: /cgn2_6/ptodata/2/pna/US099B_COMB.seq; * 42: /cgn2_6/ptodata/2/pna/US099B_COMB.seq; * 44: /cgn2_6/ptodata/2/pna/US09B_COMB.seq; * 44: /cgn2_6/ptodata/2/pna/US09B_COMB.seq; * 44: /cgn2_6/ptodata/2/pna/US000C_COMB.seq; * 44: /cgn2_6/ptodata/2/pna/US000C_COMB.seq; * 47: /cgn2_6/ptodata/2/pna/US000C_COMB.seq; * 47: /cgn2_6/ptodata/2/pna/US000C_COMB.seq; * 47: /cgn2_6/ptodata/2/pna/US000C_COMB.seq; * 55: /cgn2_6/ptodata/2/pna/US000C_COMB.seq; * 67: /cgn2_6/ptodata/2/pna/US001C_COMB.seq; * 67: /cgn2_6/ptodata/2/pna/US003C_COMB.seq; * 67: /cgn2_6/ptodata/2/p
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMAKIES

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|-------|-------|-------|-----------|----|----------------------|-------------------|
| esult | | Query | | | | |
| No. | Score | Match | Length DB | BB | ID | Description |
| 1 | 1046 | 100.0 | 618 | 33 | 33 US-09-864-921-181 | Sequence 181, App |
| N | 1046 | 100.0 | 1395 | 27 | US-09-686-347-98 | Sequence 98, Appl |
| ω | 1046 | 100.0 | 1395 | ယ | US-09-864-921-98 | Sequence 98, Appl |
| 4 | 1046 | 100.0 | 2950 | ᆫ | PCT-US00-35017A-416 | Sequence 416, App |
| ۍ | 1046 | 100.0 | 3072 | ᆫ | PCT-US00-29643-3 | Sequence 3, Appli |
| 6 | 1046 | 100.0 | 3072 | 27 | 27 US-09-697-089-3 | Sequence 3, Appli |
| | | | | | | |

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APPLICANT: Reed, John C.
APPLICANT: Pio, Frederick F.
APPLICANT: Godzik, Adam
APPLICANT: Stehlik, Christian
APPLICANT: Lee, Sug-Hyung
APPLICANT: Lee, Sug-Hyung
APPLICANT: Lee, Sug-Hyung
APPLICANT: Hayashi, Hideki
APPLICANT: Hayashi, Hideki
APPLICANT: Hayashi, Hideki
APPLICANT: Pawlowski, Krzysztof
TITLE OF INVENTION: Novel Card Domain Containing
TITLE OF INVENTION: Novel Card Domain Containing
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TITLE OF INVENTION: Novel Card Domain Containing
TITLE OF INVENTION: Polypeptides, Encoding Nucleic Acids, and
FILER REFERENCE: P-LJ 4752
CURRENT APPLICATION NUMBER: US/09/864,921
CURRENT APPLICATION NUMBER: US 09/579,240
PRIOR APPLICATION NUMBER: US 09/586,347
PRIOR APPLICATION NUMBER: US 09/686,347
PRIOR PILING DATE: 2001-03-14
NUMBER OF SEG ID NOS: 195
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 1
US-09-864-921-181
; Sequence 181, Applic
; GENERAL INFORMATION:
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  LENGTH: 618
TYPE: DNA
ORGANISM: Homo
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Sequence 98, Application US/09686347
GENERAL INFORMATION:
APPLICANT: Reed, John C.
APPLICANT: Pio, Frederick F.
APPLICANT: Oliveita, Vasco A.
APPLICANT: Oliveita, Vasco A.
APPLICANT: Lee, Sug Hyung
APPLICANT: Stehik, Christian
TITLE OF INVENTION: Novel Card-Domain Containing
TITLE OF INVENTION: Novel Card-Domain Containing
FILE REFERENCE: P-LJ 4271
CURRENT APPLICATION NUMBER: US/09/686,347
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PRIOR APPLICATION NUMBER: US 09/579, PRIOR FILING DATE: 2000-05-24

CURRENT FILING DATE:

2000-10-10

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; LOCATION: (277)...(1353)
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Sequence 98, Application US/09864921 GENERAL INFORMATION: APPLICANT: Reed, John C.
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TYPE: DNA
ORGANISM: Homo s
FEATURE:
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SOFTWARE: FastSEQ for Windows
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APPLICANT: Oliveira, Vasco A.
APPLICANT: Oliveira, Vasco A.
APPLICANT: Hayashi, Hideki
APPLICANT: Pawlowski, Krzysztof
TITLE OF INVENTION: Novel Card Domain Containing
TITLE OF INVENTION: Novel Card Domain Containing
TITLE OF INVENTION: Polypeptides, Encoding Nucleic
FILE REFERENCE: P-LJ 4752
CURRENT APPLICATION NUMBER: US/09/864,921
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 09/579,240
PRIOR APPLICATION NUMBER: US 09/579,240
PRIOR APPLICATION NUMBER: US 09/686,347
PRIOR APPLICATION NUMBER: US 09/686,347
PRIOR APPLICATION NUMBER: US 09/686,347
PRIOR FILING DATE: 2000-10-10
PRIOR FILING DATE: 2001-03-14
NUMBER OF SEO ID NOS: 195
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; NAME/KEY: CDS
; LOCATION: (277)...(1353)
US-09-864-921-98
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LENGTH: 1395
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ORGANISM: Homo
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                            LysAspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGluGlnLeu
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CURRENT FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US09/488,725
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US09/552,317
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 1478
SEQ ID NO 416
LENGTH: 2950
TYPE: DNA
ORGANISM: Homo sapiens
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TITLE OF INVENTION: Novel Nucleic Acids
FILE REFERENCE: 784PCT
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 CATTTGGAGGAGGTCCCACAACTCGTCAAGCTTGGGTTGAAAAACTGGAGACTCACAGAT
            HisLeuGluGluValProGlnLeuValLysLeuGlyLeuLysAsnTrpArgLeuThrAsp 160
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Query Match:
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PCT-US00-29643-3
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APPLICANT: Millennium
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TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATIVE OF INVENTION: PROTEIN FAMILY AND USES THEREOF FILE REFERENCE: 07334-136W01
CURRENT APPLICATION NUMBER: PCT/US00/29643
CURRENT FILING DATE: 2000-10-26
PRIOR APPLICATION NUMBER: US 60/161,822
PRIOR FILING DATE: 1999-10-27
NUMBER OF SEQ ID NOS: 11
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                                                           ThrAlaLeuMetLeuProTrpGlyCysAspValGlnGlySerLeuSerSerLeuLeuLys
                                                                                                            LysAspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGluGlnLeu
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TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
FILE REFERENCE: 07334-136001
CURRENT EXPLICATION NUMBER: US/09/697,089
CURRENT APPLICATION NUMBER: US/09/697,089
ERIOR APPLICATION NUMBER: US/09/697,089
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NUMBER OF SEQ ID NOS: 12
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TYPE: DNA
ORGANISM: Homo sapiens
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APPLICANT: Bertin, John
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PRIOR FILING DATE: 2000-10-26
PRIOR APPLICATION NUMBER: US 60/161,822
PRIOR FILING DATE: 1999-10-27
NUMBER OF SEQ ID NOS: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED FILE REFERENCE: 07334-329001 CURRENT APPLICATION NUMBER: US/09/841,739 CURRENT FILING DATE: 2001-08-29
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TYPE: DNA
ORGANISM: Homo
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TYPE: DNA
ORGANISM: Homo
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CURRENT FILING DATE: 2002-05-24
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 4.0
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TITLE OF INVENTION: IPAF, AN ICE-PROTEASE
TITLE OF INVENTION: FACTOR
FILE REFERENCE: 480140.477
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SEQ ID NO 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: 07334-136W01
CURRENT APPLICATION NUMBER: PCT/US00/29643
CURRENT FILING DATE: 2000-10-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Millennium Pnarmaceutteas, TITLE OF INVENTION: NOVEL MOLECULES OF TITLE OF INVENTION: PROTEIN FAMILY AND OTTAL 136001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/161,822 PRIOR FILING DATE: 1999-10-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: CDS
LOCATION: (36)...(3107)
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LysAspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGluGlnLeu 120
                                            GlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeuGlu 100
                                                                                         CTTGAAGAAATTCAATTAGTCTCCTGCTGCTTGTCTGCAAATGCAGTGAAAATCCTAGCT
                                                                                                      LeuGluGluIleGlnLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeuAla 80
                                                                                                                                                                 SerAspIleGlyGluGlyMetAspTyrIleValLysSerLeuSerSerGluProCysAsp 60
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GENERAL INFORMATION:
APPLICANT: Bertin, John
APPLICANT: Robison, Keith E.
                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/697,089
CURRENT FILING DATE: 2000-10-26
PRIOR APPLICATION NUMBER: US 60/161,822
PRIOR EILING DATE: 1999-10-27
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSEQ for Windows Version 4.0
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TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
FILE REFERENCE: 07334-136001
                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo
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LENGTH: 3133
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          LeuGluGluIleGlnLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeuAla 80
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Pred. No.:
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; NAME/KEY: CDS
; LOCATION: (36)...(3107)
US-09-841-739-1
                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: NOVEL MOLECULES OF THE C FILE REFERENCE: 07334-329001
CURRENT APPLICATION NUMBER: US(09/841,739)
CURRENT FILING DATE: 2001-08-29
PRIOR APPLICATION NUMBER: US 09/697,089
PRIOR FILING DATE: 2000-10-26
PRIOR APPLICATION NUMBER: US 60/161,822
PRIOR FILING DATE: 1999-10-27
NUMBER OF SEQ ID NOS: 16
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SEQ ID NO 1
LENGTH: 3133
TYPE: DNA
ORGANISM: Homo sapiens
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APPLICANT: Bertin, John
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EARLIER FILING DATE: 1999-01-20
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EARLIER APPLICATION NUMBER: US 09/240,371
EARLIER APPLICATION NUMBER: US 09/240,371
EARLIER FILING DATE: 1999-01-29
EARLIER FILING DATE: 1999-03-25
EARLIER FILING DATE: 1999-03-25
EARLIER FILING DATE: 1999-03-18
EARLIER APPLICATION NUMBER: US 09/271,490
EARLIER FILING DATE: 1999-03-18
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EARLIER FILING DATE: 1999-03-18
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EARLIER FILING DATE: 1999-03-26
EARLIER FILING DATE: 1999-05-07
EARLIER APPLICATION NUMBER: US 09/306,350
EARLIER APPLICATION NUMBER: US 09/306,350
EARLIER APPLICATION NUMBER: US 09/399,720
EARLIER APPLICATION NUMBER: US 09/404,284
EARLIER APPLICATION NUMBER: US 09/404,284
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CURRENT FILING DATE: 1999-12-23
EARLIER APPLICATION NUMBER: US 09/235,076
EARLIER FILING DATE: 1999-01-20
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                       Sequence 23, Application PC/TUS0107143
GENERAL INFORMATION:
APPLICANT: SMITHKLINE BEECHAM CORPORATION
APPLICANT: SMITHKLINE BEECHAM P.1.c.
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GP50016
CURRENT APPLICATION NUMBER: PCT/US01/07143
          CURRENT
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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (20)...(1903)
; OTHER INFORMATION: similar to
; OTHER INFORMATION: Run with F7
US-09-471-275-7095
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APPLICATION NUMBER: PCT/US01/07143 FILING DATE: 2001-03-08

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PRIOR FILING DATE: 2000-03-06
PRIOR APPLICATION NUMBER: 60/236,874
PRIOR APPLICATION NUMBER: 60/236,874
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/188,916
PRIOR FILING DATE: 2000-03-13
PRIOR APPLICATION NUMBER: 60/237,846
PRIOR FILING DATE: 2000-10-03
NUMBER OF SEQ ID NOS: 52
SOFTWARE: FastSEQ for Windows Version SEQ ID NO 23
LENGTH: 3213
TANNA 3213
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ORGANISM: Homo sapiens
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; ORGANISM: Homo
US-10-221-097-23
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PRIOR APPLICATION UMBER: 903-05
PRIOR PPLICATION UMBER: 60/187,107
PRIOR PILING DATE: 2000-03-06
PRIOR APPLICATION NUMBER: 60/236,874
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/188,916
PRIOR APPLICATION NUMBER: 60/188,916
PRIOR APPLICATION NUMBER: 60/237,846
PRIOR APPLICATION NUMBER: 60/237,846
PRIOR FILING DATE: 2000-10-03
PRIOR PRIOR PRIOR DATE: 2000-10-03
NUMBER OF SEO ID NOS: 52
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LENGTH: 3213
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APPLICANT: Agarwal, Pankaj
APPLICANT: Murdock, Paul
APPLICANT: Rizvi, Safia K
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CURRENT APPLICATION NUMBER: US/10/221,097
CURRENT FILING DATE: 2002-09-06
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APPLICANT: Smith, Randall F.
APPLICANT: Xiang, Zhaoying
TITLE OF INVENTION: NOVEL COMPOUNDS
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GENERAL INFORMATION:
APPLICANT: Alnemri, Emad S.
TITLE OF INVENTION: IPAF, AN ICE-PROTEASE ACTIVATING
TITLE OF INVENTION: FACTOR
FILE REFERENCE: 480140.477
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 14
LENGTH: 3219
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SOFTWARE: FastSEQ for Windows Version
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                                LysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHisLeu
       ThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPheGlnGln 180
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Search completed: January 31, 2003, 17:55:37 Job time : 2600.61 secs

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Listing first 45 summaries
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/cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq:*
/cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*
/cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:*
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ALIGNMENTS

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                Query Match:
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                                                                                            Alignment Scores:
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GENERAL INFORMATION:
APPLICANT: Thomas Jefferson University
APPLICANT: Alnemri, Emad S.
TITLE OF INVENTION: IPAF, AN ICE-PROTEASE ACTIVATING
TITLE OF INVENTION: FACTOR
FILE REFERENCE: 480140.477PC
                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 14

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 1
                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: PCT/US02/21946A CURRENT FILING DATE: 2002-05-24
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TYPE: DNA
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SEQ ID NO 14
LENGTH: 3219
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                                                                                                                                                                                                      FILE REFERENCE: 480140.477PC
CURRENT APPLICATION NUMBER: F
CURRENT FILING DATE: 2002-05
NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                                              APPLICANT: Thomas Jefferson University APPLICANT: Alnemri, Emad S. TITLE OF INVENTION: IPAF, AN ICE-PROTEASE TITLE OF INVENTION: FACTOR
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ORGANISM: Homo
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                                                                                                  Score:
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                                                                                                                                                                                  SOFTWARE: Fast
SEQ ID NO 111
LENGTH: 3545
                                                                                                                                                                                                                APPLICANT: Hyseq, Inc.
APPLICANT: Tang et al.
APPLICANT: Tang et al.
TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
FILE REFERENCE: 21272-018 (785 contig)
CURRENT APPLICATION NUMBER: US/10/276,781
CURRENT FILING DATE: 2002-11-18
PRIOR APPLICATION NUMBER: 09/491,404
PRIOR FILING DATE: 2000-01-25
NUMBER OF SEQ ID NOS: 2018
                                                                                                                                                                                                                                                                                                                                  Sequence 111, Application US/10276781 GENERAL INFORMATION:
                                                                                                                                                           TYPE: DNA
ORGANISM: Homo
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LeuLysAsnLeuThrLysLeuTleMetAspAsnTleLysMetAsnGluGluAspAlaTle
                                                                                                                          Scores:
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PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR APPLICATION UMBER: US 60/207,456
PRIOR FILING DATE: 04 February 2000 (04.02.00)
PRIOR PRIOR PLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 25 May 2000 (25.05.00)
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 03 October 2000 (03.10.00)
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR PRIOR PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR PRIOR PRIOR DATE: 21 September 2000 (21.09.00)
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR PRIOR PRIOR DATE: 30 June 2000 (30.06.00)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 4
US-10-203-138A-4307
; Sequence 4307, Appli; GENERAL INFORMATION:
NUMBER OF SEQ ID NOS: 15438
SOFTWARE: Molecular Dynamics Sequence 1.4~~1200 ID NO 4307
                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/203,138A CURRENT FILING DATE: 2002-08-02
                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL TITLE OF INVENTION: ANALYSIS OF GENE EXPRESSION IN BT 474
                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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Chen, Wensheng
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Rank, David R
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                     Sequence Listing Engine
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                                  CURRENT APPLICATION NUMBER: US/10/161,493
CURRENT FILING DATE: 2002-06-03
PRIOR APPLICATION NUMBER: 60/295,607
PRIOR FILING DATE: 2001-06-04
PRIOR APPLICATION NUMBER: 60/337,524
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/296,404
PRIOR APPLICATION NUMBER: 60/296,404
PRIOR APPLICATION NUMBER: 60/296,404
PRIOR APPLICATION NUMBER: 60/296,404
PRIOR FILING DATE: 2001-06-06
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                                                                                                                                                                            TITLE OF INVENTION: Novel Antibodies that Bind to Antigenic Polypeptides, Nucleic TITLE OF INVENTION: Acids Encoding the Antigens, and Methods of Use FILE REFERENCE: 21402-377A
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OTHER INFORMATION:
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Voss, Edward Z
Boldog, Ferenc L
Malyankar, Uriel M
Padigaru, Muralidhara
Ji, Weizhen
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Miller, Charles E
Shenoy, Suresh G
Hjalt, Tord
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Edinger, Shlomit R
Millet, Isabelle
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Spytek, Kimberly A
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Pena, Carol EA
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DB:
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PRIOR FILING DATE: 2001-06-12
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 299
SEQ ID NO 5
LENCTH: 2142
TYPE: DNA
TYPE: DNA
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NAME/KEY: CDS
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OR FILING DATE: 2002-02-21
OR APPLICATION NUMBER: 60/297,414
OR FILING DATE: 2001-06-11
OR APPLICATION NUMBER: 60/297,573
OR APPLICATION NUMBER: 60/341,143
OR APPLICATION NUMBER: 60/341,143
OR FILING DATE: 2001-12-14
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                                                                     GGAGAAAATGATCTTCAGGATGATGGAGTGAAGCTACTGTGTGAGGCTCTGAAACCACAT 1884
                                                                                                                                                                                                                                                                                                                                                         GCTTGCAAGCACTTGTCAGATGCTCTCCTGCAGAACAGGAGCCTGACACCCTGAATCTG
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                                                                                                                  US-09-697-089-2_COPY_762_965 (1-204) x US-10-194-163-263 (1-8722)
                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                              ; SEQUENCE
US-10-194-163-263
                                                                                                                                                                       Query Match:
                                                                                                                                                                                                                                            Pred. No.:
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APPLICANT: ROSS, Bru
TITLE OF INVENTION:
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INFORMATION FOR SEQ ID NO: 263
SEQUENCE CHARACTERISTICS:
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                                                                                   1 LeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluGluAspAlaIle
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FILING DATE: 04-Nov-2002
CLASSIFICATION: <UDknown>
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Diskette
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ADDRESSEE: MORRISON & FOERSTER

STREET: 755 PAGE MILL ROAD
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LysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPhe--
                                                                                                                                                                                                                                                                                                                                                                                                  ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 1120
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                                                   CTGGAACGTCTCACTTCGTTAACAAAGCTTCGTCTAAGAAGTAACCAGATCAGTAAACTA 2352
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STATE: CA
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; TYPE: DNA
; ORGANISM: Homo sa
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                                                                                                                           Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 19376, Application GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                     SEQ ID NO 19376
                                                                                                                                                                                                                                                                                               APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILLING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
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APPLICANT: Compugen LTD
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative
FILE REFERENCE: 129181.4 Compugen
CURRENT FILLHG DATE: 2000-11-28
CURRENT FILLHG DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
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RESULT 9
US-09-724-676-19370
US-09-724-676-19370, Application US/09724676;
GENERAL INFORMATION:
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TITLE OF INVENTION: Variants of alternative
FILE REFERENCE: 129181.4 Compugen
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CURRENT FILLING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
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APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative spl
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 19370
LENGTH: 945
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                                                               GlnGlnLeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTrpLeuAlaPheMetGly
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Sequence 19364, Application US/09724676
GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 19364
LENGTH: 1012
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US-09-724-676-19364
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Sequence 19364, Application US/09724676A
GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative:
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
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Sequence 19382 Application US/09724676
GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative spl
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
LENGTH: 1103
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NUMBER OF SEQ ID NOS: 97222

SOFTWARE: PatentIn version 3.2

SEQ ID NO 19364

FURE: DNA

ORGANISM: Homo sapiens
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Alignment Scores:
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                                                ORGANISM: Homo sapiens
                                                                       TYPE: DNA
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Sequence 19382, Application US/09724676A
GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative spiritle REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
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LENGTH: 1132
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                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Compugen LTD TITLE OF INVENTION: Variants of alternative splicing FILE REFERENCE: 129181.4 Compugen CURRENT APPLICATION NUMBER: US/09/724,676 CURRENT FILING DATE: 2000-11-28 NUMBER OF SEQ ID NOS: 97222
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1037 ATT 1039
                                                    179 GlnGlnLeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTrpLeuAlaPheMetGly 198
::: ||| ||| |||
977 GAGGCGCTCAAGCTGGAGAGCTGCGGTGTGACATCAGACAGCTGCCGGGACCTGTGCGGC 1036
                 199 val 199
:::
                                                                                                     159 ThrAspThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPhe 178
::: :::|||:::|||
920 AATGAGGCTGGCGTCCGTGTGCCAGGCCTGAAGGACTCCCCCTGCCAG---CTG 976
                                                                                                                                                        809 AAG-----CTGCAGCTGGAGTATTGCAGCCTCTCGGCTGCCAGCTGCGAGCCCCTG 859
                                                                                                                                                                                                                             119 GlnLeuThrAlaLeuMetLeuProTrpGlyCysAspValGlnGlySerLeuSerSerLeu 138
```

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